

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:04:38 ; Search time 31.3333 Seconds
(without alignments)
151.046 Million cell updates/sec

Title: US-10-009-049-2

Perfect score: 79

Sequence: 1 SRAHSGSPRPLPVV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3954

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:**

1: sp_archaea:**

2: sp_bacteria:**

3: sp_fungi:**

4: sp_human:**

5: sp_invertebrate:**

6: sp_mammal:**

7: sp_mbc:**

8: sp_organalle:**

9: sp_phage:**

10: sp_plant:**

11: sp_rodent:**

12: sp_virus:**

13: sp_vertebrate:**

14: sp_unclassified:**

15: sp_ivirus:**

16: sp_bacteriap:**

17: sp_archaeap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	34.2	14	11 Q8CJA8	Q8CJA8 mus musculu
2	27	34.2	15	11 Q8CJA9	Q8CJA9 mus musculu
3	26	32.9	13	10 Q945C1	Q945C1 crypthecodi
4	25	31.6	14	8 Q98696	Q98696 hordeum vul
5	24	30.4	12	4 Q13865	Q13865 homo sapien
6	23	29.1	9	5 Q9TWV0	Q9TWV0 anthopleura
7	23	29.1	10	12 Q8JV78	Q8JV78 polyomaviru
8	23	29.1	13	11 Q88176	Q88176 mus musculu
9	22	27.8	8	10 Q8GTG5	Q8GTG5 lycopersico
10	22	27.8	11	2 Q9EUZ3	Q9EUZ3 escherichia
11	22	27.8	13	6 Q18850	Q18850 atreles belz
12	22	27.8	14	8 Q9G3C0	Q9G3C0 calliphora
13	21.5	27.2	13	4 Q14182	Q14182 homo sapien
14	21	26.6	10	10 Q9S905	Q9S905 glycine max
15	21	26.6	13	7 Q9TNQ8	Q9TNQ8 homo sapien
16	21	26.6	15	4 Q9UCC2	Q9UCC2 homo sapien

17	21	26.6	15	4 Q00604	Q00604 homo sapien
18	20	25.3	9	4 Q16220	Q16220 homo sapien
19	20	25.3	9	11 Q9QWT0	Q9QWT0 mus musculu
20	20	25.3	11	2 Q7X566	Q7X566 thermus the
21	20	25.3	12	11 Q9QVK4	Q9QVK4 rattus sp.
22	20	25.3	14	4 Q95179	Q95179 homo sapien
23	20	25.3	15	10 P82439	P82439 nicotiana t
24	20	25.3	15	11 Q9QZC9	Q9QZC9 mus musculu
25	19.5	24.7	13	5 Q818F3	Q818F3 drosophila
26	19	24.1	9	3 Q9P8E5	Q9P8E5 kluyveromyc
27	19	24.1	9	4 Q9H4M8	Q9H4M8 homo sapien
28	19	24.1	10	11 Q9QVF7	Q9QVF7 rattus sp.
29	19	24.1	12	4 Q9EZ49	Q9EZ49 homo sapien
30	19	24.1	12	11 Q8R2F6	Q8R2F6 rattus norv
31	19	24.1	13	4 Q9UJ73	Q9UJ73 homo sapien
32	19	24.1	13	11 Q9QVK6	Q9QVK6 rattus sp.
33	19	24.1	15	2 Q9R5Z5	Q9R5Z5 streptococc
34	19	24.1	15	3 Q9UR63	Q9UR63 emericella
35	19	24.1	15	7 Q9TNQ1	Q9TNQ1 mus sp. bet
36	19	24.1	15	10 Q40562	Q40562 nicotiana t
37	19	24.1	15	10 Q40563	Q40563 nicotiana t
38	19	24.1	15	10 Q65177	Q65177 mesembryant
39	19	24.1	15	11 Q9QVC4	Q9QVC4 rattus norv
40	18	22.8	9	2 P83157	P83157 anabaena sp
41	18	22.8	9	10 Q988J8	Q988J8 oryza eativ
42	18	22.8	9	11 Q8CG39	Q8CG39 rattus norv
43	18	22.8	10	2 Q83YL7	Q83YL7 acinetobact
44	18	22.8	10	8 Q8WBR7	Q8WBR7 chaetophoru
45	18	22.8	10	12 Q8JV84	Q8JV84 polyomaviru

ALIGNMENTS

RESULT 1

Q8CJA8 PRELIMINARY; PRT; 14 AA.
ID Q8CJA8
AC Q8CJA8; DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Methylentetrahydrofolate reductase short isoform (Fragment).
GN MTHFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=22257759; PubMed=12370778;
RA Tran P., Leclerc D., Chan M., Pai A., Hiou-Tim F., Wu Q., Goyette P.,
RA Artigas C., Milos R., Rozen R.;
RA "Multiple transcription start sites and alternative splicing in the
RT methylenetetrahydrofolate reductase gene result in two enzyme
RT isoforms."
RL Mamm. Genome 13:483-492(2002).
DR EMBL; AF404271; AAN40873.1; -.
DR MGD; MGI:106639; Mthfr.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1472 MW; 28DD341AC1695CB8 CRC64;

Query Match 34.2%; Score 27; DB 11; Length 14;
Best Local Similarity 45.5%; Pred. No. 8.7e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 SRAHSGSPRP 11

Db 3 NEARGSGSPNP 13

RESULT 2

Q8CJA9

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ID O8CUA9 PRELIMINARY; PRT; 15 AA.
AC O8CUA9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE DE Methylenetetrahydrofolate reductase short isoform (Fragment).
GN MTHFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=22257759; PubMed=12370778;
RA Tran P., Leclerc D., Chan M., Pai A., Hiou-Tim F., Wu Q., Goyette P.,
RA Atligas C., Milos R., Rozen R.;
RT "Multiple transcription start sites and alternative splicing in the
RT methylenetetrahydrofolate reductase gene result in two enzyme
RT isoforms.";
RL Mamm. Genome 13:483-492(2002).
DR EMBL; AF404270; AAN40872.1; -.
DR MGD; MGI:106639; Mthfr.
FT NON TER 15
FT SEQUENCE 15 AA; 1559 MW; 8D78DD341AC1695C CRC64;
SQ
Query Match 34.2%; Score 27; DB 11; Length 15;
Best Local Similarity 45.5%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 SRAHFGSPRP 11
Db : |||||
3 NEARGSGSPNP 13

RESULT 3
ID Q945C1 PRELIMINARY; PRT; 13 AA.
AC Q945C1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Dips protein (Fragment).
OS Cryptocodium cohnii (Dinoflagellate).
OC Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Cryptocodiniaceae;
OC Cryptocodium.
OX NCBI_TaxID=2866;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21428164; PubMed=11545436;
RA Guillebaud D., Derelle E., Bhaud Y., Moreau H.;
RT "Role of nuclear WW domains and proline-rich proteins in
RT dinoflagellate transcription.";
RL Prociat 152:127-138(2001).
DR EMBL; AF417570; AAL15908.1; -.
FT NON TER 13
FT SEQUENCE 13 AA; 1225 MW; 322FA05EE70CB327 CRC64;
SQ
Query Match 32.9%; Score 26; DB 10; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 SFGSPRLP 13
Db : |||||
2 SSGPKSLP 10

RESULT 4
ID O98696 PRELIMINARY; PRT; 14 AA.
AC O98696;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ORF321 protein (Fragment).
OS Hordeum vulgare (Barley).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hassan; TISSUE=Leaf;
RX MEDLINE=20133023; PubMed=10666448;
RA del Campo E., Sabater B., Martin M.;
RT "Transcripts of the ndhD operon of barley plastids: possible role of
RT unedited site III in splicing of the ndhA intron.";
RL Nucleic Acids Res. 28:1092-1098(2000).
DR EMBL; AJ011848; CAA09818.1; -.
DR GO; GO:0009507; C:Chloroplast; IEA.
KW Chloroplast.
FT NON TER 1
FT SEQUENCE 14 AA; 1521 MW; 361CF5911A68F8B8 CRC64;
SQ
Query Match 31.6%; Score 25; DB 8; Length 14;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 HSPGS 8
Db : |||||
4 HSYGS 8

RESULT 5
ID Q13865 PRELIMINARY; PRT; 12 AA.
AC Q13865;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Kinesin light chain.
GN BETA-KINESIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=97101110; PubMed=8945637;
RA Chernaiovsky Y., Brown A., Jones T.A.;
RT "Promoter first exon/intron characterization and chromosomal location
RT of the human light chain (beta) kinesin gene.";
RL DNA Cell Biol. 15:965-974(1996).
DR EMBL; X69558; CAA49349.1; -.
DR PIR; S43170; S43170.
FT SEQUENCE 12 AA; 1274 MW; 3FB8D34EE165A5B8 CRC64;
SQ
Query Match 30.4%; Score 24; DB 4; Length 12;
Best Local Similarity 55.6%; Pred. No. 2.3e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 RAHSGSPR 10
Db : |||||
3 RGGSGGAPR 11

RESULT 6
ID Q9TWV0 PRELIMINARY; PRT; 9 AA.
AC Q9TWV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Antho-RPAMIDE=NEUROPEPTIDE.

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OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthaeae; Actiniidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN [1]
 RN SEQUENCE.
 RX MEDLINE=93126143; PubMed=1480510;
 RA Carstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;
 RT "Isolation of Leu-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH2 (Ancho-RPamide),
 an N-terminally protected, biologically active neuropeptide from sea
 anemones.";
 RL Peptides 13:851-857(1992).
 SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 29.1%; Score 23; DB 5; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 PRPLP 13
 DB 3 PGPLP 7

RESULT 7
 Q8JUV78 PRELIMINARY; PRT; 10 AA.

AC Q8JUV78;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE Large T antigen (Fragment).
 DE Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=USAL;
 RX MEDLINE=21465052; PubMed=11581397;
 RA Bofill-Mas S., Forniga-Cruz M., Clemente-Casares P., Calafell F.,
 Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 gastrointestinal tract after exposure to virions or viral DNA.";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL; AF303946; AAM97796.1; -;
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1183 MW; 4CD6A96731A32763 CRC64;

Query Match 29.1%; Score 23; DB 12; Length 10;
 Best Local Similarity 50.0%; Pred. No. 2.9e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGSPRPLP 13
 DB 1 FKXPKTLP 8

RESULT 8

O88176 PRELIMINARY; PRT; 13 AA.

AC O88176;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Neural cell adhesion molecule (Fragment).
 GN NCAM1 OR NCAM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Balb-c; TISSUE=Liver;
 RX MEDLINE=98250618; PubMed=9582442;

RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
 RT "A cis-acting regulatory element that affects the alternative splicing
 of a muscle-specific exon in the mouse NCAM gene.";
 RL Biochim. Biophys. Acta 1397:305-315(1998).
 DR EMBL; AB001873; BAA31275.1; -;
 DR MGD; MGI:97281; NCAM1.
 FT NON TER 1
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 29.1%; Score 23; DB 11; Length 13;
 Best Local Similarity 80.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PLPVV 15
 DB 3 PLPVL 7

RESULT 9

O8GTG5 PRELIMINARY; PRT; 8 AA.

AC Q8GTG5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DE WKY transcription factor Iid-1 splice variant 2 (Fragment).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Money Maker; TISSUE=Leaf;
 RA Cagna G., Boes A., Ulker B., Zhou A., Wanke D., Somasich I.E.;
 RT "Comparison of WRKY group II transcription factors from plants.";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AV157059; AAN71729.1; -;
 FT NON TER 1
 SQ SEQUENCE 8 AA; 917 MW; 5917784775B87330 CRC64;

Query Match 27.8%; Score 22; DB 10; Length 8;
 Best Local Similarity 80.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GSRP 11
 DB 3 GSPYP 7

RESULT 10

O9EUZ3 PRELIMINARY; PRT; 11 AA.

AC O9EUZ3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Ribosome binding factor A (Fragment).
 GN RBFA.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=IQ490;
 RA Hedegaard J., Kristensen J.E., Nakamura Y., Sperling-Petersen H.U.,
 Mortensen K.K.;
 RT "Sequence of the infB gene from Escherichia coli strain IQ489 and
 IQ490.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ132862; CAC20133.1; -;

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FT NON TER 11 11
SQ SEQUENCE 11 AA; 1319 MW; 6B2334CFE740879CB CRC64;

Query Match 27.8%; Score 22; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 4.6e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 AHSFGSPR 10
| | | | |
Db 2 AKFGRPQ 9

RESULT 11

018890 PRELIMINARY; PRT; 13 AA.
AC 018890;
DT 01-JAN-1998 (T-EMBLrel. 05, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Granzyme B (Fragment).
OS Ateles belzebuth chamek (Chamek spider monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles.
OX NCBI_TaxID=118643;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98267189; PubMed=9601975;
RA Canavez F., Moreira M.A.M., Borvicino C.R., Parham P., Seunarez H.N.;
RT "Comparative gene assignment in Ateles paniscus chamek (Platyrrhini, Primates) and man: association of three separate human syntenic groups and evolutionary considerations.";
RT and evolutionary considerations.";
RL Chromosoma 107:73-79(1998).
DR EMBL; AF029165; AAB84196.1; -.
DR GO; GO:0004295; P:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
FT NON TER 1
FT NON TER 13
SQ SEQUENCE 13 AA; 1394 MW; C0FF86BFBF4E5EDDD CRC64;

Query Match 27.8%; Score 22; DB 6; Length 13;
Best Local Similarity 66.7%; Pred. No. 5.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AHSFGS 8
| | | | |
Db 7 AHCWGS 12

RESULT 12

Q9G3C0 PRELIMINARY; PRT; 14 AA.
AC Q9G3C0;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Cytochrome oxidase subunit 2 (fragment).
GN COII.
OS Calliphora hilli hilli.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=145457;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ABTC3152;
RA Wallman J.F., Donnellan S.C.;
RT "The utility of mitochondrial DNA sequences for the identification of forensically-important blowflies (Diptera: Calliphoridae) in southeastern Australia.";
RT Forensic Sci. Int. 0:0-0(2001).

DR EMBL; AY012565; AAG42941.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 14 AA; 1720 MW; B659D9D3D460BFC6 CRC64;

Query Match 27.8%; Score 22; DB 8; Length 14;
Best Local Similarity 80.0%; Pred. No. 5.9e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HSFSGS 8
| | | | |
Db 2 HSFSS 6

RESULT 13

Q14182 PRELIMINARY; PRT; 13 AA.
AC Q14182;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Deoxynucleotidyltransferase (Fragment).
GN DMTT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87213162; PubMed=3579900;
RA Kawai O., Kaneda T., Morishita R.;
RT "Analysis of human terminal deoxynucleotidyl transferase cDNA RT expressible in mammalian cells.";
RL Biochem Biophys. Res. Commun. 144:185-190(1987).
DR EMBL; M26144; AAA74588.1; -.
DR PIR; I84603; I84603.
DR GO; GO:0016740; F:transferase activity; IEA.
FT NON TER 13
FT NON TER 13
SQ SEQUENCE 13 AA; 1442 MW; 25B7D365F34FC408 CRC64;

Query Match 27.2%; Score 21.5; DB 4; Length 13;
Best Local Similarity 45.5%; Pred. No. 6.7e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 7 GSP---RELTV 14
| | | | |
Db 2 GQDGRQPLPM 12

RESULT 14

Q9S905 PRELIMINARY; PRT; 10 AA.
AC Q9S905;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE S3 peptide (fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE.
RX MEDLINE=92232221; PubMed=1368037;
RA Hirano H., Kagawa K., Okubo K.;
RL Phytochemistry 31:731-735(1992).
FT NON TER 1
FT NON TER 10
SQ SEQUENCE 10 AA; 975 MW; 3C733271A879D1B7 CRC64;

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Query Match 26.6%; Score 21; DB 10; Length 10;
Best Local Similarity 60.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SPGSP 9
Db 4 TFGTP 8

RESULT 15

Q9TNQ8 PRELIMINARY; PRT; 13 AA.
AC Q9TNQ8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE HLA-A2 associated peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92212461; PubMed=1557127;
RA Wei M.L., Cresswell P.;
RT "HLA-A2 molecules in an antigen-processing mutant cell contain signal
sequence-derived peptides.";
RL Nature 356:443-446(1992).
DR PIR; I38246; I38246.
KW MHC.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1355 MW; 3E111BA716EA1768 CRC64;

Query Match 26.6%; Score 21; DB 7; Length 13;
Best Local Similarity 55.6%; Pred. No. 8.1e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 GSPRPLPVV 15
Db 5 GPRGILLAV 13

Search completed: April 2, 2004, 10:11:06
Job time : 32.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:06:43 ; Search time 14 Seconds
(without alignments)
55.314 Million cell updates/sec

Title: US-10-009-049-2

Perfect score: 79

Sequence: 1 SRAHSFGSPRLP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 146418

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pap.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pap.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pap.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pap.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pap.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	46.8	15	1 US-08-230-047-30	Sequence 30, Appl
2	35	44.3	13	3 US-08-602-999A-92	Sequence 92, Appl
3	35	44.3	13	4 US-08-278-865-92	Sequence 92, Appl
4	35	44.3	13	4 US-09-500-124-92	Sequence 92, Appl
5	34	43.0	9	4 US-09-086-168B-3	Sequence 3, Appl
6	34	43.0	11	1 US-08-336-343A-29	Sequence 29, Appl
7	34	43.0	11	3 US-08-652-877-29	Sequence 29, Appl
8	34	43.0	11	3 US-08-476-515A-29	Sequence 17, Appl
9	34	43.0	11	4 US-09-845-917A-17	Sequence 17, Appl
10	34	43.0	12	3 US-08-602-999A-255	Sequence 255, Appl
11	34	43.0	12	4 US-09-500-124-255	Sequence 255, Appl
12	34	43.0	15	3 US-08-602-999A-410	Sequence 410, Appl
13	34	43.0	15	4 US-09-500-124-410	Sequence 410, Appl
14	33	41.8	13	3 US-08-602-999A-86	Sequence 86, Appl
15	33	41.8	13	4 US-08-278-865-86	Sequence 86, Appl
16	33	41.8	13	4 US-09-500-124-86	Sequence 86, Appl
17	33	41.8	14	3 US-08-602-999A-62	Sequence 62, Appl
18	33	41.8	14	4 US-08-278-865-62	Sequence 62, Appl
19	33	41.8	14	4 US-09-500-124-62	Sequence 62, Appl
20	31	39.2	12	1 US-07-756-250-3	Sequence 3, Appl
21	31	39.2	14	3 US-08-602-999A-67	Sequence 67, Appl
22	31	39.2	14	4 US-08-278-865-67	Sequence 67, Appl
23	31	39.2	14	4 US-09-500-124-67	Sequence 67, Appl
24	31	39.2	15	1 US-08-230-047-29	Sequence 29, Appl
25	30	38.0	11	1 US-08-336-343A-24	Sequence 24, Appl
26	30	38.0	11	3 US-08-652-877-34	Sequence 34, Appl
27	30	38.0	11	3 US-08-652-877-36	Sequence 36, Appl

28	30	38.0	11	3 US-08-476-515A-34	Sequence 34, Appl
29	30	38.0	11	3 US-08-476-515A-36	Sequence 36, Appl
30	30	38.0	12	3 US-08-602-999A-281	Sequence 281, Appl
31	30	38.0	12	4 US-09-500-124-281	Sequence 281, Appl
32	30	38.0	13	3 US-08-602-999A-85	Sequence 85, Appl
33	30	38.0	13	4 US-08-278-865-85	Sequence 85, Appl
34	30	38.0	13	4 US-09-500-124-85	Sequence 85, Appl
35	30	38.0	15	3 US-08-602-999A-301	Sequence 301, Appl
36	30	38.0	15	3 US-08-602-999A-355	Sequence 355, Appl
37	30	38.0	15	4 US-09-500-124-301	Sequence 301, Appl
38	30	38.0	15	4 US-08-765-783A-83	Sequence 83, Appl
39	29	36.7	9	2 US-09-416-557-83	Sequence 83, Appl
40	29	36.7	12	4 US-09-688-188B-78	Sequence 78, Appl
41	29	36.7	12	4 US-09-688-188B-114	Sequence 114, Appl
42	29	36.7	12	4 US-09-391-417D-78	Sequence 78, Appl
43	29	36.7	12	4 US-09-391-417D-114	Sequence 114, Appl
44	29	36.7	15	3 US-08-602-999A-378	Sequence 378, Appl
45	29	36.7	15	3 US-08-602-999A-378	Sequence 378, Appl

ALIGNMENTS

RESULT 1
US-08-230-047-30
; Sequence 30, Application US/08230047
; Patent No. 5541109
; GENERAL INFORMATION:
; APPLICANT: Searioss III, George H.
; APPLICANT: Ivashchenko, Yuri D.
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230,047
; FILING DATE: 19-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A1465-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-230-047-30

Query Match 46.8%; Score 37; DB 1; Length 15;
Best Local Similarity 70.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 HSFSGSPRLP 13
DB 1 HSHFPRPLP 10

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; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,865
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-278-865-92

Query Match 44.3%; Score 35; DB 4; Length 13;
Best Local Similarity 62.5%; Pred. No. 30;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLPVV 15
DB 2 TPRPLPLI 9

RESULT 4
US-09-500-124-92
; Sequence 92, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996

; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,865
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-278-865-92

Query Match 44.3%; Score 35; DB 3; Length 13;
Best Local Similarity 62.5%; Pred. No. 30;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLPVV 15
DB 2 TPRPLPLI 9

RESULT 3
US-08-278-865-92
; Sequence 92, Application US/08278865
; Patent No. 6303574
; GENERAL INFORMATION:
; APPLICANT: SPARKS, ANDREW B.
; APPLICANT: KAY, BRIAN K.
; APPLICANT: THORN, JUDITH M.
; APPLICANT: QUILLIAM, LAWRENCE A.
; APPLICANT: DER, CHANNING J.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.

```

```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-92

Query Match 44.3%; Score 35; DB 4; Length 13;
Best Local Similarity 62.5%; Pred. No. 30;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLPV 15
DB 2 TPRPLPI 9

RESULT 5
US-09-086-168B-3
; Sequence 3, Application US/09086168B
; Patent No. 6638941
; GENERAL INFORMATION:
; APPLICANT: Castelhamo, Arlindo
; APPLICANT: Witter, David
; TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED PEPTIDOMIMETICS AS BETA-TURN
; TITLE OF INVENTION: TEMPLATES AND MODULATORS OF SH3 DOMAINS
; FILE REFERENCE: 60384-B
; CURRENT APPLICATION NUMBER: US/09/086,168B
; CURRENT FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SH3 test peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Synthetic Peptide
US-09-086-168B-3

Query Match 43.0%; Score 34; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
DB 1 PRPLPV 6

RESULT 6
US-08-336-343A-29
; Sequence 29, Application US/08336343A
; Patent No. 5677144
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Alves, Frauke
; TITLE OF INVENTION: CKK-2, A No. 5677144el Receptor Tyrosine Kinase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
```

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;
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,343A
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-336-343A-29

Query Match 43.0%; Score 34; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
DB 2 PRPLPV 7

RESULT 7
US-08-652-877-29
; Sequence 29, Application US/08652877
; Patent No. 6187548
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjaln, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd., 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.5.1
; SOFTWARE: Word 6.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,877
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/US95/15203
; APPLICATION NUMBER:
; FILING DATE: 22-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
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;; FILING DATE: 23-NOV-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/487,314
;; FILING DATE: 07-JUNE-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Savitzky, Martin
;; REGISTRATION NUMBER: 29,699
;; REFERENCE/DOCKET NUMBER: A1355E-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-454-3816
;; TELEFAX: 610-454-3808
;; INFORMATION FOR SEQ ID NO: 29:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; FRAGMENT TYPE: internal
US-08-652-877-29
Query Match 43.0%; Score 34; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 PRPLPV 14
Db 2 PRPLPV 7
RESULT 8
US-08-476-515A-29
; Sequence 29, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjaln, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Martin Savitzky
; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
; STREET: 3C43,
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 7.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,515A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE94/00483
; FILING DATE: 24-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9301764-8
; FILING DATE: 24-MAY-1993
; ATTORNEY/AGENT INFORMATION:

;; NAME: Savitzky, Martin
;; REGISTRATION NUMBER: 29,699
;; REFERENCE/DOCKET NUMBER: A1355D
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-454-3816
;; TELEFAX: 610-454-3808
;; INFORMATION FOR SEQ ID NO: 29:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; FRAGMENT TYPE: internal
US-08-476-515A-29
Query Match 43.0%; Score 34; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 PRPLPV 14
Db 2 PRPLPV 7
RESULT 9
US-09-845-917A-17
; Sequence 17, Application US/09845917A
; Patent No. 6653529
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845,917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PPT
; ORGANISM: Caenorhabditis elegans
US-09-845-917A-17
Query Match 43.0%; Score 34; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 PRPLPV 14
Db 2 PRPLPV 7
RESULT 10
US-08-602-999A-255
; Sequence 255, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOMKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 255:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-255

Query Match 43.0%; Score 34; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PRPLPV 14
Db 3 PRPLPV 8

RESULT 11
US-09-500-124-255
Sequence 255, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999

FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 255:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-255

Query Match 43.0%; Score 34; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PRPLPV 14
Db 3 PRPLPV 8

RESULT 12
US-08-602-999A-410
Sequence 410, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 410:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-410

Query Match 43.0%; Score 34; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
| | | | |
Db 4 PRPLPV 9

RESULT 13

US-09-500-124-410
; Sequence 410, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 410:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-410

Query Match 43.0%; Score 34; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
| | | | |
Db 4 PRPLPV 9

RESULT 14

US-08-602-999A-86
; Sequence 86, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-86

Query Match 41.8%; Score 33; DB 3; Length 13;
Best Local Similarity 62.5%; Pred. No. 59;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLPV 15
| | | | |
Db 2 TPRPLPV 9

RESULT 15

US-08-278-865-86
; Sequence 86, Application US/08278865
; Patent No. 6303574
; GENERAL INFORMATION:

APPLICANT: KAY, BRIAN K.
APPLICANT: SPARKS, ANDREW B.
APPLICANT: THORN, JUDITH M.
APPLICANT: QUILLIAM, LAWRENCE A.
APPLICANT: DER, CHANNING J.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IEM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,865
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-278-865-86

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Query Match 41.8%; Score 33; DB 4; Length 13;
Best Local Similarity 62.5%; Pred. No. 59;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY      8 SPRLPVV 15
Db      2 TPRPLPML 9

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Search completed: April 2, 2004, 10:12:45
Job time : 15 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 2, 2004, 10:05:03 ; Search time 11 Seconds
(without alignments)
131.170 Million cell updates/sec

Title: US-10-009-049-3

Perfect score: 82

Sequence: 1 CRAHSFVSPRLPVV 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2522

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78: *

1: PIR1: *

2: PIR2: *

3: PIR3: *

4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	35.4	14	2 S27140	hypothetical prote
2	25	30.5	12	2 S01122	photosystem II 3.7
3	24	29.3	10	2 I44644	neurotoxin-associ
4	23	28.0	9	4 S15594	orf 1 rara 5'-regi
5	23	28.0	13	1 XAVI9B	angiotensin-conver
6	23	28.0	15	2 PA0060	protein QF200037 -
7	22	26.8	13	2 PL0157	ig kappa chain V-I
8	21	25.6	7	2 S42620	aggreccan - bovine
9	21	25.6	10	2 XGHUE	erythrocyte membra
10	21	25.6	11	2 C61497	seed protein ws-18
11	21	25.6	13	2 S01119	photosystem II pro
12	21	25.6	13	2 JH0460	corticostatic pept
13	21	25.6	13	2 S36668	hypothetical prote
14	21	25.6	14	2 S12904	protein kinase (EC
15	21	25.6	15	2 A35232	gentisate 1,2-diox
16	21	25.6	15	2 PX0031	mixed lymphocyte r
17	20	24.4	10	2 PX0030	triacylglycerol li
18	20	24.4	13	2 PA0089	protein QF200053 -
19	20	24.4	13	2 I84603	deoxynucleotidyltr
20	20	24.4	15	2 A40634	orf19 3' of eryk
21	20	24.4	15	2 S62641	porphobilinogen sy
22	19	23.2	9	2 A31576	xylose isomerase (
23	19	23.2	10	1 XAVI6B	angiotensin-conver
24	19	23.2	10	2 A43977	EMRamide-like pro
25	19	23.2	11	1 XASNBA	bradykinin-potenti
26	19	23.2	11	2 JN0023	substance P - chic
27	19	23.2	11	2 S23308	substance P - rain
28	19	23.2	11	2 S23306	substance P - Atla
29	19	23.2	11	2 S33300	probable substance

30	19	23.2	11	2 C37196	bradykinin-potenti
31	19	23.2	11	2 D37196	bradykinin-potenti
32	19	23.2	14	2 PA0104	protein QF200070 -
33	19	23.2	14	2 PH1614	ig H chain V-D-J r
34	19	23.2	15	2 B39109	hypothetical 1.5K
35	19	23.2	15	2 A60929	dichloromethane de
36	19	23.2	15	2 B60929	dichloromethane de
37	19	23.2	15	2 PA0027	protein QA100006 -
38	19	23.2	15	2 A32921	beaded-chain filam
39	19	23.2	15	2 B32800	hypothetical prote
40	18.5	22.6	12	2 PA0098	ribosomal protein
41	18	22.0	8	2 S10783	enamelin f - bovin
42	18	22.0	8	2 PH1618	ig H chain V-D-J r
43	18	22.0	10	2 C39745	sphingomyelinase -
44	18	22.0	10	2 S71948	matrix metalloprot
45	18	22.0	11	2 S66196	alcohol dehydrogen

ALIGNMENTS

RESULT 1

S27140
hypothetical protein 1 estrogen receptor 5'-region - human
C:Species: Homo sapiens (man)
C>Date: 05-Mar-1994 #sequence_revision 12-May-1995 #text_change 18-Aug-2000
C:Accession: S27140
R:Keaveney, M.; Klug, J.; Gannon, F.
DNA Seq. 2, 347-358, 1992

A>Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene.
A:Reference number: S27140; MUID:93075998; PMID:1476547
A:Accession: S27140
A>Status: translation not shown
A:Residues: 1-14 <KEA>

A:Molecule type: DNA
A:Cross-references: EMBL:X62462; NID:G31201; PIDN:CAA44319.1; PID:G31202
C:Superfamily: unassigned leader peptides

Query Match 35.4%; Score 29; DB 2; Length 14;
Best Local Similarity 54.5%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 RAHSFVSPRLP 12
DB 2 RAHSFLPSHSL 12

RESULT 2

S01122
photosystem II 3.7K protein - spinach (fragment)
C:Species: Spinacia Oleracea (spinach)
C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C:Accession: S01122
R:Schroeder, W.P.; Henrysson, T.; Akerlund, H.E.
FEBS Lett. 235, 289-292, 1988

A>Title: Characterization of low molecular mass proteins of photosystem II by N-terminal
A:Reference number: S01120
A:Accession: S01122
A:Molecule type: protein
A:Residues: 1-12 <SCH>

C:Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

Query Match 30.5%; Score 25; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 5.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 AHSFVSP 9
DB 5 AYAFUSP 11

RESULT 3

I44644

neurotoxin-associated protein type B Hn+ 57K chain - Clostridium botulinum (fragment)
 C;Species: Clostridium botulinum
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
 C;Accession: I44644
 R;Somers, E.; DasGupta, B.R.
 J. Protein Chem. 10, 415-425, 1991
 A;Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without he
 A;Reference number: A44644; MUID:92143938; PMID:1781887
 A;Contents: type B
 A;Accession: I44644
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <SOM>
 A;Note: sequence extracted from NCBI backbone (NCBIP:83783)
 C;Keywords: hemagglutinin

Query Match 29.3%; Score 24; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 6.7e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 FVSPRLP 13
 DB 2 FVTQVLP 9

RESULT 4
 S15594
 orf 1 rara 5'-region - human
 C;Species: Homo sapiens (man)
 C;Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
 C;Accession: S15594
 R;Brand, N.J.; Petkovich, M.; Chambon, P.
 Nucleic Acids Res. 18, 6799-6806, 1990
 A;Title: Characterization of a functional promoter for the human retinoic acid receptor-
 A;Reference number: S15594; MUID:91088249; PMID:2175878
 A;Accession: S15594
 A;Molecule type: DNA
 A;Residues: 1-9 <BRA>
 A;Cross-references: EMBL:X56057; NID:q35875
 A;Note: this ORF from Fig. 2 is not annotated in GenBank entry HSRARAL, release 111.0
 C;Comment: This sequence is not thought to be translated.
 C;Genetics:
 A;Gene: GDB:RARA
 A;Cross-references: GDB:120337; OMIM:180240
 A;Map position: 17q12-17q12

Query Match 28.0%; Score 23; DB 4; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 VSPRP 11
 DB 5 IAPRP 9

RESULT 5
 XAVI9B
 angiotensin-converting enzyme inhibitor V-9 - jararaca
 C;Species: Bothrops jararaca (jararaca)
 C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995
 C;Accession: A01253
 R;Ondetti, M.A.; Williams, N.J.; Sabo, E.F.; Pluscec, J.; Weaver, E.R.; Kocoy, O.
 Biochemistry 10, 4033-4039, 1971
 A;Title: Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. I
 A;Reference number: A90356; MUID:72118526; PMID:4334402
 A;Accession: A01253
 A;Molecule type: protein
 A;Residues: 1-13 <OND>
 A;Note: the structure of the peptide was confirmed by synthesis
 C;Comment: This peptide also potentiates bradykinin by inhibiting the kinases that inact
 C;Superfamily: bradykinin-potentiating peptide
 C;Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 28.0%; Score 23; DB 1; Length 13;
 Best Local Similarity 57.1%; Pred. No. 1.3e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 PRPLPV 15
 DB 5 PRPGPEI 11

RESULT 6
 PA0060
 protein QP200037 - fungus (Fusarium sporotrichioides) (fragment)
 C;Species: Fusarium sporotrichioides
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C;Accession: PA0060
 R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich:
 A;Reference number: PA0051
 A;Accession: PA0060
 A;Molecule type: protein
 A;Residues: 1-15 <CHO>

Query Match 28.0%; Score 23; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 RPLP 13
 DB 3 RPLP 6

RESULT 7
 PL0157
 Ig kappa chain V-II region (anti-myelin-associated glycoprotein, PEC) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-Feb-1997
 C;Accession: PL0157; C61458
 R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
 J. Exp. Med. 170, 1551-1558, 1989
 A;Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-asso-
 A;Reference number: A61458; MUID:90039128; PMID:2478651
 A;Accession: PL0157
 A;Molecule type: protein
 A;Residues: 1-13 <BRO>
 A;Accession: C61458
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-13 <BR2>
 C;Comment: This protein is one of monoclonal IGM reactive with myelin-associated glycopro-
 C;Keywords: glycoprotein; heterotrimer; immunoglobulin

Query Match 26.8%; Score 22; DB 2; Length 13;
 Best Local Similarity 71.4%; Pred. No. 1.9e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 SPRPLPV 14
 DB 7 SPVTLEPV 13

RESULT 8
 S42620
 aggrecan - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
 C;Accession: S42620
 R;Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.
 Matrix Biol. 14, 171-179, 1994
 A;Title: Aggrecan in bovine tendon.
 A;Reference number: S42620; MUID:94340214; PMID:7520336
 A;Accession: S42620

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C;Date: 30-Jun-1989 #sequence_revision 31-Dec-1990 #text_change 19-Jan-1990
C;Accession: S01119
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QY 1 CFAHSEVSPRP 11
DB : : : :
2 CEGRRRTTSP 12

RESULT 14

S12904
protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)
C:Species: Pisaster ochraceus
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C:Accession: S12904
R:Sanghera, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.
F885 Lett. 273, 223-226, 1990
A:Title: Identification of the sites in myelin basic protein that are phosphorylated by
A:Reference number: S12904; PMID:91032186; PMID:1699809
A:Accession: S12904
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <SAN>
C:Keywords: phosphotransferase

Query Match 25.6%; Score 21; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. NO. 2.9e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 SFVSPRPLP 13
DB : : : :
1 NIVTPRTP 9

RESULT 15

A35232
genitrate 1,2-dioxygenase (EC 1.13.11.4) - Comamonas testosteroni (fragment)
C:Species: Comamonas testosteroni
C>Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 23-Jun-1993
C:Accession: A35232
R:Harpel, M.R.; Lipscomb, J.D.
J. Biol. Chem. 265, 6301-6311, 1990
A:Title: Genitrate 1,2-dioxygenase from Pseudomonas. Purification, characterization, and
A:Reference number: A35232; PMID:90202907; PMID:2156846
A:Accession: A35232
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <HAR>
C:Keywords: oxidoreductase

Query Match 25.6%; Score 21; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. NO. 3.1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 VSPRPLPV 14
DB : : : :
3 VQAQXPV 10

Search completed: April 2, 2004, 10:11:51
Job time : 11 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 2, 2004, 09:58:38 ; Search time 7.66667 Seconds
(without alignments)
101.876 Million cell updates/sec

Title: US-10-009-049-3
Perfect score: 82
Sequence: 1 CRAHSFVSPRLPVV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 801

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	31.7	15	UC29_MAIZE	P80635 zea mays (m
2	24	29.3	9	FAR9_ASCSU	P43172 ascaris suu
3	24	29.3	15	MK1_PALPR	P80408 palomena pr
4	24	29.3	15	MK2A_PALPR	P80409 palomena pr
5	23	28.0	12	BP4_PERFU	P82690 periplaneta
6	23	28.0	13	BP4_BOTJA	P01020 bothrops ja
7	22	26.8	12	BP4_PERAM	P82619 periplaneta
8	21	25.6	10	GLEM_HUMAN	P02728 homo sapien
9	21	25.6	11	TIN4_HOFTI	P82654 hoplobatr
10	21	25.6	12	TIN2_HOFTI	P82652 hoplobatr
11	21	25.6	12	TIN3_HOFTI	P82653 hoplobatr
12	20	24.4	9	MGMT_BOVIN	P29177 bos taurus
13	19	23.2	9	XILA_STRSQ	P19149 streptomyce
14	19	23.2	10	BPP2_BOTJA	P01022 bothrops ja
15	19	23.2	10	FARP_MANSE	P18523 manduca sex
16	19	23.2	11	BPP3_BOTIN	P30423 bothrops in
17	19	23.2	11	BPP4_BOTIN	P30424 bothrops in
18	19	23.2	11	BPPB_AKSHA	P01021 agkistrodon
19	19	23.2	11	TKNA_CHICK	P19850 gallus gall
20	19	23.2	11	TKNA_GADMO	P28498 gadus morhu
21	19	23.2	11	TKNA_ONCMY	P28499 oncorhynch
22	19	23.2	11	TKNA_SCYCA	P41333 scyllorhinu
23	19	23.2	13	ECDE_LYMDI	P80941 lymantria d
24	19	23.2	14	UC15_MAIZE	P80621 zea mays (m
25	19	23.2	15	CX3B_CONQU	P38842 conus querc
26	18	22.0	13	TEMD_RANTE	P56919 rana tempor
27	18	22.0	13	UP51_UPFIN	P82036 uperoleia i
28	18	22.0	14	ECDC_LYMDI	P80940 lymantria d
29	18	22.0	15	CLOA_RAT	P31720 rattus norv
30	18	22.0	15	LM42_LOCHI	P38497 locusta mig
31	18	22.0	15	UC16_MAIZE	P80622 zea mays (m
32	17	20.7	10	TKU1_UREUN	P40751 urechis uni
33	17	20.7	10	TMOF_AEDAE	P19425 aedes aegy

34	17	20.7	11	TIN1_HOFTI	P82651 hoplobatr
35	17	20.7	11	TKNA_HORSE	P01290 equus cabal
36	17	20.7	12	CXL3_CONMR	P58809 conus marmo
37	17	20.7	13	CRBL_VESLE	P17235 vespula lew
38	17	20.7	13	CRBL_VESMA	P17232 vespa manda
39	17	20.7	13	CRBL_VESXA	P17234 vespa xanth
40	17	20.7	13	GER1_HORVU	P28525 hordeum vul
41	17	20.7	13	GER2_HORVU	P28526 hordeum vul
42	17	20.7	13	PEDI_HVDAT	P80578 hydra atten
43	17	20.7	13	TEME_RANTE	P56920 rana tempor
44	17	20.7	14	EFTU_CANFA	P54935 canis famil
45	17	20.7	14	UHA1_CANFA	P99503 canis famil

ALIGNMENTS

RESULT 1
UC29_MAIZE
ID UC29_MAIZE STANDARD; PRT; 15 AA.
AC P80635;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 45) (Fragment).
DE Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 4.9, its MW is: 37.6 kDa.
CC Maize-2DPAGE; P80635; COLEOPTILE.
DR MaizeDB; 123960; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1679 MW; 3D53086B16018BC1 CRC64;

Query Match 31.7%; Score 26; DB 1; Length 15;
Best Local Similarity 42.9%; Pred. No. 2.5e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 SPRPLPV 14
:|:|:
Db 1 NPNEVPI 7

RESULT 2
FAR9_ASCSU
ID FAR9_ASCSU STANDARD; PRT; 9 AA.
AC P43172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRamide-like neuropeptide AF9.
OC Ascaris suum (Fig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stratton A.O.W.;
RT "Eight novel FMRamide-like neuropeptides isolated from the nematode

RT Ascaris suum.;
 RL Peptides 16:491-500(1995).
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide) family.
 CC Neuropeptide; Amidation.
 FT MOD RES 9 9
 SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 29.3%; Score 24; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 VSPRPL 12
 : ||||
 Db 2 LGPRPL 7

RESULT 3
 MK1_PALPR STANDARD; PRT; 15 AA.
 AC P80408;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Metanikowin I.
 OS Palomena prasina (Green shield bug).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
 OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
 CC Palomena.
 OC NCBI_TaxID=55431;
 RN [1]
 RP TISSUE=Hemolymph;
 RC Cherrysh S. Cociancich S., Briand J.-P., Hetru C., Bulet P.;
 RA "The inducible antibacterial peptides of the hemipteran insect
 RT Palomena prasina: Identification of a unique family of proline-rich
 RT peptides and of a novel insect defensin."
 RL J. Insect Physiol. 42:81-89(1996).
 CC -1- FUNCTION: Antibacterial peptide active against Gram-negative
 CC bacteria.
 CC -1- INDUCTION: By bacterial infection.
 CC Antibiotic; Insect immunity.
 KW SEQUENCE 15 AA; 1838 MW; 21407E663CE46299 CRC64;

Query Match 29.3%; Score 24; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 5.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 PRPLP 13
 : ||||
 Db 8 PRPRP 12

RESULT 4
 MK2A_PALPR STANDARD; PRT; 15 AA.
 AC P80409;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Metanikowin IIA.
 OS Palomena prasina (Green shield bug).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
 CC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
 CC Palomena.
 OC NCBI_TaxID=55431;
 RN [1]
 RP TISSUE=Hemolymph;
 RC Cherrysh S. Cociancich S., Briand J.-P., Hetru C., Bulet P.;
 RA "The inducible antibacterial peptides of the hemipteran insect

RT Palomena prasina: identification of a unique family of proline-rich
 RL peptides and of a novel insect defensin."
 CC -1- FUNCTION: Antibacterial peptide active against Gram-negative
 CC bacteria.
 CC -1- INDUCTION: By bacterial infection.
 CC Antibiotic; Insect immunity.
 KW SEQUENCE 15 AA; 1893 MW; 23835D063B946299 CRC64;

Query Match 29.3%; Score 24; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 5.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 PRPLP 13
 : ||||
 Db 8 PRPRP 12

RESULT 5
 PK4_PERFU STANDARD; PRT; 12 AA.
 AC P82630;
 DT 18-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-4 (PFF-PK-4) (YXPRL-amide).
 OS Periplaneta fuliginosa (Smokybrown cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;
 OC Blattellidae; Periplaneta.
 OC NCBI_TaxID=36977;
 RN [1]
 RP TISSUE=FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Gamma-specific distribution of FXPRLAMides in the nervous system of
 RT the American cockroach."
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -1- MASS SPECTROMETRY: MW=1437.9; METHOD=MALDI.
 CC -1- SIMILARITY: Belongs to the Pyrokinin family.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; FALSE NEG.
 KW Neuropeptide; Amidation; Pyrokinin_5
 FT MOD RES 12 12
 SQ SEQUENCE 12 AA; 1439 MW; F9B53049FF42CAAL CRC64;

Query Match 28.0%; Score 23; DB 1; Length 12;
 Best Local Similarity 50.0%; Pred. No. 6.2e+02;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 AHSFVSPP 10
 : ||||
 Db 4 SHDVYSPP 11

RESULT 6
 BPPI_BOTJA STANDARD; PRT; 13 AA.
 AC P01020; P30421;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S3.1 (13A) (Angiotensin-converting
 DE enzyme inhibitor V-9).
 OS Bothrops jararaca (Jararaca), and
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Sceleroglossa; Serpentes; Colubroidea;
 CC Viperidae; Crotalinae; Bothrops.
 OC NCBI_TaxID=8724, 8723;

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RN RP SEQUENCE.
RC SPECIES=B.jararaca; TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=B.insularis; TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01253; XAVI9B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1388 MW; 6824FC97D83D6774 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 13;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 PRPLPVV 15
    |||||
DB 5 PRGPEI 11

RESULT 7
PPK4 PERAM
ID _PPK4_PERAM STANDARD; PRT; 12 AA.
AC P82619;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-4 (Pea-PK-4) (YXPRU-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Retrocerebral complex.
RX MEDLINE=99212459; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinin-isoforms in cerebral and
RT abdominal neurohemal organs of the American cockroach.";
RL Insect Biochem. Mol. Biol. 29:139-144(1999).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRlamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- TISSUE SPECIFICITY: Corpora cardiaca.
CC -1- MASS SPECTROMETRY: MW=1147.9; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the pyrokinin family.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1449 MW; FA7A3049FF42CAA1 CRC64;

Query Match 26.8%; Score 22; DB 1; Length 12;

Best Local Similarity 57.1%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 HSFVSPR 10
    |||||
DB 5 HDVYSPR 11

RESULT 8
GLEM HUMAN
ID _GLEM_HUMAN STANDARD; PRT; 10 AA.
AC P02728;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythrocyte membrane glycopeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72034940; PubMed=5286858;
RA Weiss J.B., Lote C.J., Bobinski H.;
RT "New low molecular weight glycopeptide containing triglucoylcysteine
RT in human erythrocyte membrane.";
RL Nature New Biol. 234:25-26(1971).
CC -1- PTM: S-linked glycan consists of GLC-GLC-Glc trisaccharide.
CC -1- MISCELLANEOUS: The identity of the glycoprotein from which this
CC peptide is derived is unknown. No physiological function has been
CC attributed.
DR PIR; A03187; XGHUE.
KW Glycoprotein; Erythrocyte.
FT CARBOHYD 1 1 S-LINKED (GLC. . .).
SQ SEQUENCE 10 AA; 1049 MW; 239BFEEA1F5B1E8 CRC64;

Query Match 25.6%; Score 21; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRAHS 5
    |||
DB 1 CEGHS 5

RESULT 9
TIN4 HOPTI
ID _TIN4_HOPTI STANDARD; PRT; 11 AA.
AC P82654;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tigerin-4.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=1031261;
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -1- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
CC S.aureus, M.luteus, P.putida and S.cerevisiae.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic.

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FT DISULFID 3 11
SQ SEQUENCE 11 AA; 1248 MW; 117D8BFD37605DCB CRC64;

Query Match 25.6%; Score 21; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PLPV 14
   |||
Db 7 PLPI 10

RESULT 10
TIN2_HOPTI STANDARD; PRT; 12 AA.
AC P82652;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tigerin-2.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RA "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.",
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
CC S.aureus, M.luteus, P.putida and S.cerevisiae.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1368; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1369 MW; C2627D8BFD37605D CRC64;

Query Match 25.6%; Score 21; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PLPV 14
   |||
Db 7 PLPI 10

RESULT 11
TIN3_HOPTI STANDARD; PRT; 12 AA.
AC P82653;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tigerin-3.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RA "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
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RT tigerina.",
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
CC S.aureus, M.luteus, P.putida and S.cerevisiae.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1409; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1411 MW; C0717D8BFD37605D CRC64;

Query Match 25.6%; Score 21; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PLPV 14
   |||
Db 7 PLPI 10

RESULT 12
MGMT_BOVIN STANDARD; PRT; 9 AA.
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-
DE methylguanine-DNA methyltransferase) (fragment).
GN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=90174912; PubMed=2308822;
RA Rydberg B., Hall J., Karran P.;
RA "Active site amino acid sequence of the bovine O6-methylguanine-DNA
RT methyltransferase.",
RL Nucleic Acids Res. 18:17-21(1990).
CC -!- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically
CC transferring the alkyl group at the O-6 position to a cysteine
CC residue in the enzyme. This is a suicide reaction: the enzyme is
CC irreversibly inactivated.
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + protein
CC [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein
CC S-methyl-L-cysteine.
CC -!- SIMILARITY: WITH SEGMENTS OF E.COLI ADA AND OCT METHYLTRANSFERASE
CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
DR InterPro; IPR001497; Methyltransf 1.
DR PROSITE; PS00374; MGMT; PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON_TER 1 1
FT ACT_SITE 9 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 24.4%; Score 20; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 11 PLPV 15
   |||
Db 2 PIPIL 6

RESULT 13
XYLA_STRSQ STANDARD; PRT; 9 AA.
ID XYLA_STRSQ
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P19149;
 01-NOV-1990 (Rel. 16, Created)
 01-NOV-1990 (Rel. 16, Last sequence update)
 10-OCT-2003 (Rel. 42, Last annotation update)
 Xylose isomerase (EC 5.3.1.5) (Fragment).
 XYL4.
 GN Streptomyces sp. (strain NCL 82-5-1).
 OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OC NCB1_TaxID=1931;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88326335; PubMed=3415697;
 RA Pawar H.S., Kannan K., Srinivasan M.C., Vartak H.G.;
 RT "Purification and characterisation of glucose (xylose) isomerase from
 Chainia sp. (NCL 82-5-1).";
 RL Biochem. Biophys. Res. Commun. 155:411-417(1988).
 CC -!- FUNCTION: Involved in D-xylose catabolism.
 CC -!- CATALYTIC ACTIVITY: D-xylose = D-xylulose.
 CC -!- COFACTOR: Binds 2 magnesium ions per subunit (Potential).
 CC -!- SUBUNIT: Homotetramer.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the xylose isomerase family.
 DR PIR; A31576; A31576.
 DR HAWAP; MF_00455; -; 1.
 DR InterPro; IPR001998; Xylose isom.
 DR PROSITE; PS00172; Xylose isomerase 1; PARTIAL.
 DR PROSITE; PS00173; Xylose isomerase 2; PARTIAL.
 KW Isomerase; Pentose shunt; Xylose metabolism; Metal-binding; Magnesium.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 983 MW; F64BA1EDCSB87DD1 CRC64;
 Query Match 23.2%; Score 19; DB 1; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 AHSP 6
 Db 6 AHFT 9
 RESULT 14
 ID BPP2 BOTJA STANDARD; PRT; 10 AA.
 AC P01022;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme
 inhibitor V-6-II).
 DE Bothrops jararaca (Jararaca).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OC NCB1_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Venom;
 RA MEDLINE=72118526; PubMed=4334402;
 RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
 RA Kocy O.;
 RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
 jararaca. Isolation, elucidation of structure, and synthesis.";
 RL Biochemistry 10:4033-4039(1971).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 angiotensin-converting enzyme and enhances the action of
 bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; A01255; XAVI6B.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match 23.2%; Score 19; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 9 PRP 11
 Db 4 PRP 6
 RESULT 15
 ID FARP MANSE STANDARD; PRT; 10 AA.
 AC P18523;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRFamide-like neuropeptide.
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
 OC Sphingidae; Sphinginae; Manduca.
 OC NCB1_TaxID=7130;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91045350; PubMed=2235684;
 RA Kingan T.G., Teplow D.B., Phillips J.M., Riehm J.P., Rao K.R.,
 RA Hildebrand J.G., Homberg U., Kammer A.E., Jardine I., Griffin P.R.,
 RA Hunt D.F.;
 RT "A new peptide in the FMRFamide family isolated from the CNS of the
 hawkmoth, Manduca sexta.";
 RL Peptides 11:849-856(1990).
 CC -!- FUNCTION: Increases the force of neurally evoked contractions in
 the major power-producing flight muscles, the dorsal longitudinal
 muscles and so is likely to play a role in sustaining or promoting
 flight behavior patterns.
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 family.
 DR PIR; A43977; A43977.
 KW Amidation; Neuropeptide; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1247 MW; D3C45229D5B1F2D2 CRC64;
 Query Match 23.2%; Score 19; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 HSFV 7
 Db 5 HSLF 8

Search completed: April 2, 2004, 10:09:18
 Job time : 8.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:04:38 ; Search time 31.3333 Seconds

(without alignments)
151.046 Million cell updates/sec

Title: US-10-009-049-3

Perfect score: 82

Sequence: 1 CRAHSFVSPRLPVV 15

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3954

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	30.5	15	Q95771	ctenosaura
2	25	30.5	15	Q95952	sauromalus
3	25	30.5	15	Q95879	phrynosoma
4	25	30.5	15	Q95770	cyclura ric
5	24	29.3	10	Q95829	clostridium
6	23	28.0	9	Q95829	anthopleura
7	23	28.0	9	Q95829	rattus norv
8	23	28.0	10	Q95829	polyomaviru
9	23	28.0	13	Q95829	mus musc
10	21	25.6	11	Q95829	thermus the
11	21	25.6	11	Q95829	psophocarpu
12	21	25.6	13	Q95829	cavia (guin
13	21	25.6	15	Q95829	homo sapien
14	21	25.6	15	Q95829	homo sapien
15	20	24.4	9	Q95829	homo sapien
16	20	24.4	9	Q95829	mus musc

17	20	24.4	12	11	Q9QVK4
18	20	24.4	12	11	Q8R2F6
19	20	24.4	13	4	Q14182
20	20	24.4	13	4	Q9UJ52
21	20	24.4	14	8	Q9G3C0
22	20	24.4	15	4	Q9HCX8
23	20	24.4	15	5	Q26323
24	20	24.4	15	10	Q9S8B1
25	20	24.4	15	10	P82439
26	19.5	23.8	14	11	Q9QVF3
27	19	23.2	9	3	Q9P8E5
28	19	23.2	10	4	Q9UCO4
29	19	23.2	11	2	Q8KHL0
30	19	23.2	11	2	Q8KRAL
31	19	23.2	12	2	Q9L8H8
32	19	23.2	12	2	Q9K3B4
33	19	23.2	12	2	Q9L8H6
34	19	23.2	12	4	Q9BZ49
35	19	23.2	13	10	Q945C1
36	19	23.2	13	11	Q9QVK6
37	19	23.2	15	2	O54298
38	19	23.2	15	2	Q9R5Z5
39	19	23.2	15	3	Q9UR63
40	19	23.2	15	6	Q9TRG9
41	19	23.2	15	7	Q9TNQ1
42	19	23.2	15	10	Q941J1
43	19	23.2	15	10	Q40562
44	19	23.2	15	10	Q40563
45	18.5	22.6	9	2	P83157

ALIGNMENTS

RESULT 1

Q95771 ID Q95771 PRELIMINARY; PRT; 15 AA.
AC Q95771;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 4 (Fragment).
GN ND4.
OS Ctenosaura similis (Spiny-tailed iguana).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Ctenosaura.
OX NCBI_TaxID=51212;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97013047; PubMed=8865663;
RA Sites J.W. Jr., Davis S.K., Guerra T., Iverson J.B., Snell H.L.;
RT "Character congruence and phylogenetic signal in molecular and
RT morphological data sets: a case study in the living Iguanas (Squamata,
RT Iguanidae).";
RL Mol. Biol. Evol. 13:1087-1105(1996).
DR EMBL; U66228; AB07474.1;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 15 AA; 1853 MW; 8327178CA9352C01 CRC64;

Query Match 30.5%; Score 25; DB 8; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRAHS 5

Db 3 CRHS 7

RESULT 2

Q95952

ID Q95952 PRELIMINARY; PRT; 15 AA.
 AC Q95952;
 DT 01-FEB-1997 (TReMBLrel. 02, Created)
 DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE NADH dehydrogenase subunit 4 (Fragment).
 GN ND4.
 OS Sauromalus varius (San Esteban island chuckwalla).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Sauromalus.
 OX NCBI_TaxID=51220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97019047; PubMed=8865663;
 RA Sites J.W. Jr., Davis S.K., Guerra T., Iverson J.B., Snell H.L.;
 RT "Character congruence and phylogenetic signal in molecular and
 RT morphological data sets: a case study in the living Iguanas (Squamata,
 RT Iguanidae).";
 RL Mol. Biol. Evol. 13:1087-1105 (1996).
 DR EMBL; U66233; AAB07480.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1843 MW; 8327179CE9203901 CRC64;
 Query Match 30.5%; Score 25; DB 8; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRAHS 5
 ||||
 Db 3 CRLHS 7

RESULT 3
 Q95879 PRELIMINARY; PRT; 15 AA.
 ID Q95879;
 DT 01-FEB-1997 (TReMBLrel. 02, Created)
 DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE NADH dehydrogenase subunit 4 (Fragment).
 GN ND4.
 OS Phrynosoma cornutum (Texas horned lizard).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
 OC Phrynosoma.
 OX NCBI_TaxID=43610;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97019047; PubMed=8865663;
 RA Sites J.W. Jr., Davis S.K., Guerra T., Iverson J.B., Snell H.L.;
 RT "Character congruence and phylogenetic signal in molecular and
 RT morphological data sets: a case study in the living Iguanas (Squamata,
 RT Iguanidae).";
 RL Mol. Biol. Evol. 13:1087-1105 (1996).
 DR EMBL; U66224; AAB07478.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1767 MW; 22C713C3138D16B7 CRC64;
 Query Match 30.5%; Score 25; DB 8; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRAHS 5
 ||||
 Db 3 CRLHS 7

RESULT 4
 Q95770 PRELIMINARY; PRT; 15 AA.
 ID Q95770;
 DT 01-FEB-1997 (TReMBLrel. 02, Created)
 DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE NADH dehydrogenase subunit 4 (fragment).
 GN ND4.
 OS Cyclura ricordi (Ricord's rock iguana).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Cyclura.
 OX NCBI_TaxID=51215;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97019047; PubMed=8865663;
 RA Sites J.W. Jr., Davis S.K., Guerra T., Iverson J.B., Snell H.L.;
 RT "Character congruence and phylogenetic signal in molecular and
 RT morphological data sets: a case study in the living Iguanas (Squamata,
 RT Iguanidae).";
 RL Mol. Biol. Evol. 13:1087-1105 (1996).
 DR EMBL; U66237; AAB07473.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1715 MW; 8327178E7927A57E CRC64;
 Query Match 30.5%; Score 25; DB 8; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRAHS 5
 ||||
 Db 3 CRLHS 7

RESULT 5
 Q9RSN3 PRELIMINARY; PRT; 10 AA.
 ID Q9RSN3;
 AC Q9RSN3;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Neurotoxin type B Hn+ 57 kDa subunit (Fragment).
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92143938; PubMed=1781887;
 RA Somers E., DasGupta B.R.;
 RT "Clostridium botulinum types A, B, C1, and E produce proteins with or
 RT without hemagglutinating activity: do they share common amino acid
 RT sequences and genes?";
 RL J. Protein Chem. 10:415-425 (1991).
 DR PIR; I44644; I44644.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1221 MW; C3DBE932D416C1B2 CRC64;
 Query Match 29.3%; Score 24; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.6e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 FVSPPPLP 13
 ||||
 Db 2 FVTORVLP 9

RESULT 6
 Q9TWVO

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ID Q9TWW0 PRELIMINARY; PRT; 9 AA.
AC Q9TWW0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Antho-RPAMIDE-NEUROPEPTIDE.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nyantheae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN SEQUENCE.
RP MEDLINE=93126143; PubMed=1480510;
RA Carstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;
RT "Isolation of Leu-Pro-Gly-Pro-Leu-Arg-Pro-NH2 (Ancho-RPamide),
RT an N-terminally protected, biologically active neuropeptide from sea
RT anemones.";
RL Peptides 13:851-857(1992).
SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 28.0%; Score 23; DB 5; Length 9;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 PRPLP 13
DB 3 PGPLP 7

RESULT 7
Q8CG39 PRELIMINARY; PRT; 9 AA.
AC Q8CG39;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Histamine N-tele-methyltransferase (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN SEQUENCE FROM N.A.
RP STRAIN=Sprague-Dawley; TISSUE=Liver;
RA Takemura M., Yamauchi K., Yamatodani A.;
RT "Structural analysis of histamine N-methyltransferase gene.";
RL Methods Find. Exp. Clin. Pharmacol. 17:1-4(1995).
DR EMBL; S82579; AAN86745.1; -.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Transferase; Methyltransferase.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1060 MW; 4223B1E042CBB053 CRC64;

Query Match 28.0%; Score 23; DB 11; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRAHSF 6
DB 4 CVHSF 9

RESULT 8
Q8JV78 PRELIMINARY; PRT; 10 AA.
AC Q8JV78;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.

Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
NCBI_TaxID=10632;
RN SEQUENCE FROM N.A.
RP STRAIN=USAL;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303946; AAM97796.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1183 MW; 4CD6A96731A32763 CRC64;

Query Match 28.0%; Score 23; DB 12; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 FVSPRLP 13
DB 1 FKPKTLP 8

RESULT 9
Q88176 PRELIMINARY; PRT; 13 AA.
AC Q88176;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN NCAM1 OR NCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP STRAIN=Balb-C; TISSUE=Liver;
RA MEDLINE=98250618; PubMed=9582442;
RA Kawahigashi H., Harada Y., Aeano A., Nakamura M.;
RT "A cis-acting regulatory element that affects the alternative splicing
RT of a muscle-specific exon in the mouse NCAM gene.";
RL Biochim. Biophys. Acta 1397:305-315(1998).
DR EMBL; AB001873; BAA31275.1; -.
DR MGD; MGI:97281; Ncam1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 28.0%; Score 23; DB 11; Length 13;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PLPVV 15
DB 3 PLPVL 7

RESULT 10
Q7X566 PRELIMINARY; PRT; 11 AA.
AC Q7X566;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN
```



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RP SEQUENCE FROM N.A.
RA Miyazaki T., Miyazaki J., Nishiyama M., Yamane H.;
RT "Characterization of a lysN, the 4th enzyme in lysine biosynthesis, in
  an extremely thermophilic bacterium, Thermus thermophilus HB27."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB097117; BAC76940.1; -.
RW Hypothetical protein.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1073 MW; 39792C1E75B72EB8 CRC64;

Query Match      25.6%; Score 21; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 VSPRP 11
DB 6 LSPKP 10

RESULT 11
Q9S8Z9 ID Q9S8Z9 PRELIMINARY; PRT; 11 AA.
AC Q9S8Z9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE W1 peptide (Fragment).
OS Peptococcus tetragonolobus (Goa bean) (Asparagus bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; rosids;
OC eucotyledons I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpus.
OX NCBI_TaxID=3891;
RN [1]
RP SEQUENCE.
RX MEDLINE=92232221; PubMed=1368037;
RA Hirano H., Kagawa H., Okubo K.;
RL Phytochemistry 31:731-735(1992).
DR PIR; C61497; C61497.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1120 MW; 8391BACBD7772D1 CRC64;

Query Match      25.6%; Score 21; DB 10; Length 11;
Best Local Similarity 55.6%; Pred. No. 5.6e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 VSPRPPLPV 15
DB 1 VSPTPPVL 9

RESULT 12
Q9QVI3 ID Q9QVI3 PRELIMINARY; PRT; 13 AA.
AC Q9QVI3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE GP-GS3-CORTICOSTATIC peptide (Fragment).
OS Cavia (guinea pigs).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae.
OX NCBI_TaxID=10140;
RN [1]
RP SEQUENCE.
RX MEDLINE=92062075; PubMed=1659400;
RA Hu J., Bennett H.P., Lazure C., Solomon S.;
RT "Isolation and characterization of corticostatic peptides from guinea
  pig bone marrow."
RL Biochem. Biophys. Res. Commun. 180:558-565(1991).
FT NON_TER 1
FT NON_TER 13

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SQ SEQUENCE 13 AA; 1706 MW; D26CD1E63AA50EB9 CRC64;

Query Match      25.6%; Score 21; DB 11; Length 13;
Best Local Similarity 75.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRAH 4
DB 7 CRH 10

RESULT 13
Q9UCC2 ID Q9UCC2 PRELIMINARY; PRT; 15 AA.
AC Q9UCC2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 35 kDa heparin-RELEASABLE protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94059921; PubMed=8241100;
RA Novotny W.F., Maffi T., Mehta R.L., Milner P.G.;
RT "Identification of novel heparin-releasable proteins, as well as the
  cytokines midkine and pleiotrophin, in human postheparin plasma."
RL Arterioscler. Thromb. 13:1798-1805(1993).
SQ SEQUENCE 15 AA; 1454 MW; 0585FEF4FE8F6265 CRC64;

Query Match      25.6%; Score 21; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 PRPLPV 14
DB 5 PVPIPL 10

RESULT 14
O00604 ID O00604 PRELIMINARY; PRT; 15 AA.
AC O00604;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Type I collagen alpha 1(I) chain (Fragment).
GN COL1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96336021; PubMed=8757037;
RA Mayer S.A., Rubin B.S., Starmen B.J., Byers P.H.;
RT "Spontaneous multivessel cervical artery dissection in a patient with
  a substitution of alanine for glycine (G13A) in the alpha 1 (I) chain
  of type I collagen."
RL Neurology 47:552-556(1996).
DR EMBL; S83315; AAB50780.2; -.
KW Collagen.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1413 MW; 4CABD720AAF780FC CRC64;

Query Match      25.6%; Score 21; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 7.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 PRPLP 13

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Db 5 PRGLP 9

RESULT 15

Q16220
ID Q16220 PRELIMINARY; PRT; 9 AA.
AC Q16220;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE HGRP protein (Fragment).
GN HGRP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94320083; PubMed=8044796;
RA Nagalla S.R., Spindel E.R.;
RT "Functional analysis of the 5'-flanking region of the human gastrin-
releasing peptide gene in small cell lung carcinoma cell lines.";
RL Cancer Res. 54:4461-4467(1994).
DR EMBL; S73265; AAD14116.1; -.
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1070 MW; 77FE37672B040864 CRC64;

Query Match 24.4%; Score 20; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 10 RELPVV 15
Db 4 RELPLV 9

Search completed: April 2, 2004, 10:11:07
Job time : 32.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:06:43 ; Search time 14 Seconds
(without alignments)
55.314 Million cell updates/sec

Title: US-10-009-049-3

Perfect score: 82

Sequence: 1 CRAHSFVSPRLP15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 146418

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pap:*
 - 2: /cgn2_6/ptodata/2/iaa/5B COMB.pap:*
 - 3: /cgn2_6/ptodata/2/iaa/6A COMB.pap:*
 - 4: /cgn2_6/ptodata/2/iaa/6B COMB.pap:*
 - 5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pap:*
 - 6: /cgn2_6/ptodata/2/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	47.6	15	1	US-08-230-047-30
2	35	42.7	13	1	US-08-230-047-39
3	35	42.7	13	3	US-08-602-999A-92
4	35	42.7	13	4	US-08-278-865-92
5	35	42.7	13	4	US-09-500-124-92
6	34	41.5	9	4	US-09-086-168B-3
7	34	41.5	11	1	US-08-336-343A-29
8	34	41.5	11	3	US-08-652-877-29
9	34	41.5	11	3	US-08-476-515A-29
10	34	41.5	11	4	US-09-845-917A-17
11	34	41.5	12	1	US-08-190-788A-167
12	34	41.5	12	1	US-08-383-474B-170
13	34	41.5	12	1	US-08-465-391A-167
14	34	41.5	12	2	US-08-464-538B-167
15	34	41.5	12	2	US-08-463-076E-219
16	34	41.5	12	3	US-08-602-999A-255
17	34	41.5	12	4	US-09-500-124-255
18	34	41.5	12	4	US-09-428-082B-783
19	34	41.5	15	3	US-08-602-999A-410
20	34	41.5	15	4	US-09-500-124-410
21	33	40.2	13	3	US-08-602-999A-86
22	33	40.2	13	4	US-08-278-865-86
23	33	40.2	13	4	US-09-500-124-86
24	33	40.2	14	3	US-08-602-999A-62
25	33	40.2	14	4	US-08-278-865-62
26	33	40.2	14	4	US-09-500-124-62
27	31	37.8	14	3	US-08-602-999A-67

28	31	37.8	14	4	US-08-278-865-67	Sequence 67, Appl
29	31	37.8	14	4	US-09-500-124-67	Sequence 67, Appl
30	31	37.8	15	1	US-08-230-047-29	Sequence 29, Appl
31	31	37.8	15	3	US-08-630-916A-96	Sequence 96, Appl
32	31	37.8	15	3	US-08-602-999A-355	Sequence 355, App
33	31	37.8	15	3	US-08-602-999A-396	Sequence 396, App
34	31	37.8	15	4	US-08-630-915A-152	Sequence 152, App
35	31	37.8	15	4	US-09-500-124-355	Sequence 355, App
36	31	37.8	15	4	US-09-500-124-396	Sequence 396, App
37	30	36.6	11	1	US-08-336-343A-24	Sequence 24, Appl
38	30	36.6	11	3	US-08-652-877-34	Sequence 34, Appl
39	30	36.6	11	3	US-08-652-877-36	Sequence 36, Appl
40	30	36.6	11	3	US-08-476-515A-34	Sequence 34, Appl
41	30	36.6	11	3	US-08-476-515A-36	Sequence 36, Appl
42	30	36.6	12	1	US-08-190-788A-218	Sequence 218, App
43	30	36.6	12	1	US-08-383-474B-221	Sequence 221, App
44	30	36.6	12	1	US-08-465-391A-218	Sequence 218, App
45	30	36.6	12	2	US-08-464-538B-218	Sequence 218, App

ALIGNMENTS

RESULT 1
US-08-230-047-30
; Sequence 30, Application US/08230047
; Patent No. 5541109
; GENERAL INFORMATION:
; APPLICANT: Searfoss III, George H.
; APPLICANT: Ivashchenko, Yuri D.
; APPLICANT: Jave, Michael C.
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; STREET: Rhone-Poulenc Rorer Inc.
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230,047
; FILING DATE: 19-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A1465-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-230-047-30

Query Match 47.6%; Score 39; DB 1; Length 15;
Best Local Similarity 70.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 4 HSFVSPRLP 13
|||
Db 1 HSHFPRPLP 10

RESULT 2
 US-08-230-047-39
 ; Sequence 39, Application US/08230047
 ; Patent No. 5541109
 ; GENERAL INFORMATION:
 ; APPLICANT: Searfoss III, George H.
 ; APPLICANT: Ivashchenko, Yuri D.
 ; APPLICANT: Jaye, Michael C.
 ; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
 ; TITLE OF INVENTION: PROTEIN
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.
 ; STREET: 500 Arcola Road, 3C43
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: System 7.1
 ; SOFTWARE: Word 5.0 (PatentIn)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/230,047
 ; FILING DATE: 19-APR-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Goodman, Rosanne
 ; REGISTRATION NUMBER: 32,534
 ; REFERENCE/DOCKET NUMBER: A1465-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 454-3817
 ; TELEFAX: (610) 454-3808
 ; INFORMATION FOR SEQ ID NO: 39:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-230-047-39

Query Match 42.7%; Score 35; DB 1; Length 13;
 Best Local Similarity 70.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 HSFVSPRPLP 13
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 Db 3 HSAVPRPGP 12

RESULT 3
 US-08-602-999A-92
 ; Sequence 92, Application US/08602999A
 ; Patent No. 6184205
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; TITLE OF INVENTION: ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.

; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/602,999A
 ; FILING DATE: 16-FEB-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 1101-202
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 92:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-08-602-999A-92

Query Match 42.7%; Score 35; DB 3; Length 13;
 Best Local Similarity 62.5%; Pred. No. 13;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLPVV 15
 : ||||| :
 Db 2 TPRPLPLI 9

RESULT 4
 US-08-278-865-92
 ; Sequence 92, Application US/08278865
 ; Patent No. 6303574
 ; GENERAL INFORMATION:
 ; APPLICANT: KAY, BRIAN K.
 ; APPLICANT: SPARKS, ANDREW B.
 ; APPLICANT: THORN, JUDITH M.
 ; APPLICANT: QUILLIAM, LAWRENCE A.
 ; APPLICANT: DER, CHANNING J.
 ; TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF
 ; TITLE OF INVENTION: ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 106
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ; STREET: 1755 S. Jefferson Davis Highway, Suite 400
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/278,865
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Villacorta, Gilberto M.
 ; REGISTRATION NUMBER: 34,038
 ; REFERENCE/DOCKET NUMBER: 4980-007-0
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 413-3000
 ; TELEFAX: (703) 413-2220
 ; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 92:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-278-865-92

Query Match 42.7%; Score 35; DB 4; Length 13;
Best Local Similarity 62.5%; Pred. NO. 13;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SPRPLPV 15

Db 2 TPRPLPI 9

RESULT 5

US-09-500-124-92

; Sequence 92, Application US/09500124

; Patent No. 6432920

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/500,124

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/602,999

; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: MISROCK, S. Leelle

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 92:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-09-500-124-92

Query Match 42.7%; Score 35; DB 4; Length 13;
Best Local Similarity 62.5%; Pred. NO. 13;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SPRPLPV 15

Db 2 TPRPLPI 9

Db 2 TPRPLPI 9

RESULT 6

US-09-086-168B-3

; Sequence 3, Application US/09086168B

; Patent No. 6638941

; GENERAL INFORMATION:

; APPLICANT: Castelhamo, Arlindo

; APPLICANT: Witter, David

; TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED PEPTIDOMIMETICS AS BETA-TURN

; TITLE OF INVENTION: TEMPLATES AND MODULATORS OF SH3 DOMAINS

; FILE REFERENCE: 60384-B

; CURRENT APPLICATION NUMBER: US/09/086,168B

; CURRENT FILING DATE: 1998-05-28

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: SH3 test peptide

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)..(9)

; OTHER INFORMATION: Synthetic Peptide

US-09-086-168B-3

Query Match 41.5%; Score 34; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PRPLPV 14

Db 1 PRPLPV 6

RESULT 7

US-08-336-343A-29

; Sequence 29, Application US/08336343A

; Patent No. 5677144

; GENERAL INFORMATION:

; APPLICANT: Ullrich, Axel

; APPLICANT: Alves, Frauke

; TITLE OF INVENTION: CKK-2, A No. 5677144e1 Receptor Tyrosine Kinase

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/336,343A

; FILING DATE: 08-NOV-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7683-065

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 29:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-336-343A-29

Query Match 41.5%; Score 34; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
Db 2 PRPLPV 7

RESULT 8

US-08-652-877-29
; Sequence 29, Application US/08652877
; Patent No. 6187548
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjaln, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd., 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.5.1
; SOFTWARE: Word 6.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,877
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15203
; FILING DATE: 22-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,314
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355E-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-652-877-29

Query Match 41.5%; Score 34; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
Db 2 PRPLPV 7

RESULT 9

US-08-476-515A-29
; Sequence 29, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjaln, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Martin Savitzky
; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
; STREET: 3C43,
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 7.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,515A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE94/00483
; FILING DATE: 24-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9301764-8
; FILING DATE: 24-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-476-515A-29

Query Match 41.5%; Score 34; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14

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Db          2 PRPLPV 7
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RESULT 10
US-09-845-917A-17
; Sequence 17, Application US/09845917A
; Patent No. 6653529
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845,917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-845-917A-17

Query Match          41.5%; Score 34; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          9 PRPLPV 14
|||||
Db          2 PRPLPV 7

RESULT 11
US-08-190-788A-167
; Sequence 167, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832

US-08-190-788A-167
; INFORMATION FOR SEQ ID NO: 167:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-190-788A-167

Query Match          41.5%; Score 34; DB 1; Length 12;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy          4 HSFVSPRPLPV 14
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Db          2 HQFQPYALPL 12

RESULT 12
US-08-383-474B-170
; Sequence 170, Application US/08383474B
; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: the IL-1 Receptor
; NUMBER OF SEQUENCES: 314
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend & Townsend & Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,474B
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-383-474B-170

Query Match          41.5%; Score 34; DB 1; Length 12;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy          4 HSFVSPRPLPV 14
|||||
Db          2 HQFQPYALPL 12
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RESULT 13
US-08-465-391A-167
; Sequence 167, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,391A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786331v1el, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 167:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-391A-167

Query Match 41.5%; Score 34; DB 1; Length 12;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 HSFVSPRPLPV 14
Db 2 HQFVQPVYALPL 12

RESULT 14
US-08-464-538B-167
; Sequence 167, Application US/08464538B
; Patent No. 5861476
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.

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; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,538B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528A-001810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 167:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-464-538B-167

Query Match 41.5%; Score 34; DB 2; Length 12;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 HSFVSPRPLPV 14
Db 2 HQFVQPVYALPL 12

RESULT 15
US-08-463-076E-219
; Sequence 219, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA

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1  ZIP: 94111-3834
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3  COMPUTER READABLE FORM:
4
5  MEDIUM TYPE: Floppy disk
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7  COMPUTER: IBM PC compatible
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9  OPERATING SYSTEM: PC-DOS/MS-DOS
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11 SOFTWARE: PatentIn Release #1.0, Version #1.30
12
13 CURRENT APPLICATION DATA:
14
15 APPLICATION NUMBER: US/08/463.076E
16
17 FILING DATE: 05-JUN-1995
18
19 CLASSIFICATION: 514
20
21 ATTORNEY/AGENT INFORMATION:
22
23 NAME: Snyder, Joseph R.
24
25 REGISTRATION NUMBER: 39,381
26
27 REFERENCE/DOCKET NUMBER: 16529A-001850US
28
29 TELECOMMUNICATION INFORMATION:
30
31 TELEPHONE: (415) 576-0200
32
33 TELEFAX: (415) 576-0300
34
35 INFORMATION FOR SEQ ID NO: 219:
36
37 SEQUENCE CHARACTERISTICS:
38
39 LENGTH: 12 amino acids
40
41 TYPE: amino acid
42
43 STRANDEDNESS:
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45 TOPOLOGY: linear
46
47 MOLECULE TYPE: peptide
48
49 US-08-463-076E-219

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Query Match      41.5%; Score 34; DB 2; Length 12;
Best Local Similarity 54.3%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      4 HSFVSPRPPLPV 14
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Db       2 HQFVQPYALEL 12

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OM protein - protein search, using sw model

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Title: US-10-009-049-3

Sequence: 82

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Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	42.7	13	9	US-09-938-315-92
2	35	42.7	13	14	US-10-161-791-92
3	34	41.5	11	10	US-09-945-917-17
4	34	41.5	11	10	US-09-845-917A-17
5	34	41.5	12	12	US-10-603-217-783
6	34	41.5	12	12	US-10-632-388-783
7	34	41.5	12	12	US-10-651-723-783
8	34	41.5	12	14	US-10-161-791-255
9	34	41.5	15	14	US-10-161-791-410
10	33	40.2	9	10	US-09-999-686-22
11	33	40.2	13	9	US-09-938-315-86
12	33	40.2	13	14	US-10-161-791-86
13	33	40.2	14	9	US-09-938-315-62
14	33	40.2	14	14	US-10-161-791-62
15	31	37.8	14	9	US-09-938-315-67

16	31	37.8	14	14	US-10-161-791-67	Sequence 67, Appl
17	31	37.8	15	9	US-09-879-957-152	Sequence 152, App
18	31	37.8	15	14	US-10-185-050-96	Sequence 96, Appl
19	31	37.8	15	14	US-10-161-791-355	Sequence 355, App
20	31	37.8	15	14	US-10-161-791-396	Sequence 396, App
21	30	36.6	10	10	US-09-572-404B-1593	Sequence 1593, Ap
22	30	36.6	11	15	US-10-149-138-4631	Sequence 4631, Ap
23	30	36.6	12	12	US-10-609-217-835	Sequence 835, App
24	30	36.6	12	12	US-10-632-388-835	Sequence 835, App
25	30	36.6	12	12	US-10-651-723-835	Sequence 835, App
26	30	36.6	12	14	US-10-286-457-30	Sequence 30, Appl
27	30	36.6	12	14	US-10-161-791-281	Sequence 281, App
28	30	36.6	13	9	US-09-938-315-85	Sequence 85, Appl
29	30	36.6	13	14	US-10-161-791-85	Sequence 85, Appl
30	30	36.6	15	14	US-10-161-791-301	Sequence 301, App
31	29	35.4	11	12	US-10-398-104-192	Sequence 192, App
32	29	35.4	12	14	US-10-158-596A-14	Sequence 14, Appl
33	29	35.4	12	14	US-10-157-775B-14	Sequence 14, Appl
34	29	35.4	12	14	US-10-254-446A-14	Sequence 14, Appl
35	29	35.4	12	14	US-10-155-883B-14	Sequence 14, Appl
36	29	35.4	15	9	US-09-895-814-960	Sequence 960, App
37	29	35.4	15	13	US-10-012-896-960	Sequence 960, App
38	29	35.4	15	14	US-10-144-678A-960	Sequence 960, App
39	29	35.4	15	14	US-10-294-025-960	Sequence 960, App
40	29	35.4	15	14	US-10-232-544-68	Sequence 68, Appl
41	28.5	34.8	15	14	US-10-161-791-306	Sequence 306, App
42	28	34.1	8	9	US-09-815-837-114	Sequence 114, App
43	28	34.1	8	14	US-10-008-524A-26	Sequence 26, Appl
44	28	34.1	8	14	US-10-008-524A-27	Sequence 27, Appl
45	28	34.1	8	14	US-10-008-524A-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-938-315-92
; Sequence 92, Application US/09938315
; Patent No. US20020091085A1
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; SPARKS, ANDREW B.
; THORN, JUDITH M.
; QUILLIAM, LAWRENCE A.
; DER, CHANNING J.
; TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/938,315
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248055 OPAT UR

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; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 13 amino acids
;   TYPE: amino acid
;   TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 92:
US-09-938-315-92

Query Match      42.7%; Score 35; DB 9; Length 13;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      8 SPRPLPV 15
Db      2 TPRPLELI 9

RESULT 2
US-10-161-791-92
; Sequence 92, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: O'QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;   ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 13 amino acids
;   TYPE: amino acid
;   TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-92

Query Match      42.7%; Score 35; DB 14; Length 13;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      8 SPRPLPV 15
Db      2 TPRPLELI 9

; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 13 amino acids
;   TYPE: amino acid
;   TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 92:
US-09-945-917-17

Query Match      41.5%; Score 34; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 BRPLPV 14
Db      2 PRPLPV 7

RESULT 3
US-09-945-917-17
; Sequence 17, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
;   CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
;   PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
;   USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-945-917-17

Query Match      41.5%; Score 34; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 BRPLPV 14
Db      2 PRPLPV 7

RESULT 4
US-09-845-917A-17
; Sequence 17, Application US/09845917A
; Publication No. US20030167538A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
;   CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
;   PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
;   USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845,917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-845-917A-17

Query Match      41.5%; Score 34; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 BRPLPV 14
Db      2 PRPLPV 7

RESULT 5
US-10-609-217-783
; Sequence 783, Application US/10609217
; Publication No. US2004004188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; US-10-609-217-783
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; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 783
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-609-217-783

Query Match 41.5%; Score 34; DB 12; Length 12;
Best Local Similarity 54.5%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 HSFVSPRPLPV 14
| | | | |
Db 2 HOFVQPYALPL 12

RESULT 6
US-10-632-388-783
; Sequence 783, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 783
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-632-388-783

Query Match 41.5%; Score 34; DB 12; Length 12;
Best Local Similarity 54.5%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 HSFVSPRPLPV 14
| | | | |
Db 2 HOFVQPYALPL 12

RESULT 7
US-10-651-723-783
; Sequence 783, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.

; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 783
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-651-723-783

Query Match 41.5%; Score 34; DB 12; Length 12;
Best Local Similarity 54.5%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 HSFVSPRPLPV 14
| | | | |
Db 2 HOFVQPYALPL 12

RESULT 8
US-10-161-791-255
; Sequence 255, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/161,791
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 255:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids

;
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-255

Query Match 41.5%; Score 34; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PRPLPV 14
Db 3 PRPLPV 8

RESULT 9

US-10-161-791-410
; Sequence 410, Application US/10161791
; Publication No. US20030186863A1

; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/161,791

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA: US/08/602,999

; APPLICATION NUMBER: 16-FEB-1996

; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Mistrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 410:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-10-161-791-410

Query Match 41.5%; Score 34; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PRPLPV 14
Db 4 PRPLPV 9

RESULT 10

US-09-999-686-22

; Sequence 22, Application US/09999686
; Publication No. US20030028000A1

; GENERAL INFORMATION:
; APPLICANT: Aziz, Nazneen

; APPLICANT: Hedley, Mary Lynne

; APPLICANT: Urban, Robert G.

; APPLICANT: Tomlinson, Andrew J.

; APPLICANT: Cole, Geoffrey

; TITLE OF INVENTION: CYP1B1 NUCLEIC ACIDS AND METHODS OF USE

; FILE REFERENCE: 08191-021001

; CURRENT APPLICATION NUMBER: US/09/999,686

; CURRENT FILING DATE: 2001-10-31

; PRIOR APPLICATION NUMBER: 60/298,428

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/261,719

; PRIOR FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: 60/244,501

; PRIOR FILING DATE: 2000-10-31

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 22

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-999-686-22

Query Match 40.2%; Score 33; DB 10; Length 9;
Best Local Similarity 66.7%; Pred. No. 9.7e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FVSPRLPV 14
Db 1 FLDPRLPV 9

RESULT 11

US-09-938-315-86

; Sequence 86, Application US/09938315
; Patent No. US20020091085A1

; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.

; THORN, JUDITH M.

; QUILLIAM, LAWRENCE A.

; DER, CHANNING J.

; TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF

; ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; P.C.

; STREET: 1755 S. Jefferson Davis Highway, Suite 400

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/938,315

; FILING DATE: 23-Aug-2001

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Villacorta, Gilberto M.

; REGISTRATION NUMBER: 34,038

; REFERENCE/DOCKET NUMBER: 4980-007-0

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-938-315-86

Query Match 40.2%; Score 33; DB 9; Length 13;
Best Local Similarity 62.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLPVV 15
Db :|||||:
2 TPRPLPML 9

RESULT 12
US-10-161-791-86
; Sequence 86, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-86

Query Match 40.2%; Score 33; DB 14; Length 13;
Best Local Similarity 62.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLPVV 15
Db :|||||:
2 TPRPLPML 9

RESULT 13
US-09-938-315-62
; Sequence 62, Application US/09938315
; Patent No. US20020091085A1
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; SPARKS, ANDREW B.
; THORN, JUDITH M.
; QUILLIAM, LAWRENCE A.
; DER, CHANNING J.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,315
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-09-938-315-62

Query Match 40.2%; Score 33; DB 9; Length 14;
Best Local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLPVV 15
Db :|||||:
3 TPRPLPML 10

RESULT 14
US-10-161-791-62
; Sequence 62, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.

APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161.791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602.999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-62

Query Match 40.2%; Score 33; DB 14; Length 14;
Best Local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SPRLPVV 15
Db 3 TPRPLPML 10

RESULT 15

US-09-938-315-67
Sequence 67, Application US/09938315
Patent No. US20020091085A1
GENERAL INFORMATION:
APPLICANT: KAY, BRIAN K.
SPARKS, ANDREW B.
THORN, JUDITH M.
QUILLIAN, LAWRENCE A.
DER, CHANNING J.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938.315
FILING DATE: 23-Aug-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-007-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-938-315-67

Query Match 37.8%; Score 31; DB 9; Length 14;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SPRLPL 13
Db 3 TPRPLP 8

Search completed: April 2, 2004, 10:23:35
Job time : 32.3333 secs

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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:11:14 ; Search time 32.3333 Seconds
(without alignments)
121.720 Million cell updates/sec

Title: US-10-009-049-2

Perfect score: 79

Sequence: 1 SRAHSGSPRLPVV 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1070241 seqs, 262374223 residues

Total number of hits satisfying chosen parameters: 173041

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	44.3	13	9	US-09-938-315-92
2	35	44.3	13	14	US-10-161-791-92
3	34	43.0	11	10	US-09-945-917-17
4	34	43.0	11	10	US-09-845-917A-17
5	34	43.0	12	14	US-10-161-791-255
6	34	43.0	15	14	US-10-161-791-410
7	33	41.8	13	9	US-09-938-315-86
8	33	41.8	13	14	US-10-161-791-86
9	33	41.8	14	9	US-09-938-315-62
10	33	41.8	14	14	US-10-161-791-62
11	31	39.2	14	9	US-09-938-315-67
12	31	39.2	14	14	US-10-161-791-67
13	30	38.0	8	9	US-09-815-837-114
14	30	38.0	11	15	US-10-149-138-4631
15	30	38.0	12	14	US-10-286-457-30

16	30	38.0	12	14	US-10-161-791-281
17	30	38.0	13	9	US-09-938-315-85
18	30	38.0	13	14	US-10-161-791-85
19	30	38.0	14	10	US-09-966-459A-37
20	30	38.0	14	12	US-10-308-128-60
21	30	38.0	15	14	US-10-001-469-2561
22	30	38.0	15	14	US-10-001-469-2562
23	30	38.0	15	14	US-10-161-791-301
24	30	38.0	15	14	US-10-161-791-395
25	29	36.7	9	9	US-09-730-857-83
26	29	36.7	9	12	US-10-601-837-101
27	29	36.7	10	10	US-09-572-404B-1382
28	29	36.7	10	10	US-09-572-404B-1384
29	29	36.7	10	10	US-09-572-404B-1593
30	29	36.7	10	14	US-10-044-896-9
31	29	36.7	12	10	US-09-291-417-78
32	29	36.7	12	10	US-09-291-417-114
33	29	36.7	12	14	US-10-158-596A-14
34	29	36.7	12	14	US-10-157-775B-14
35	29	36.7	12	14	US-10-254-446A-14
36	29	36.7	12	14	US-10-155-883B-14
37	29	36.7	13	14	US-10-193-477-59
38	29	36.7	14	14	US-10-185-050-223
39	29	36.7	15	14	US-10-161-791-378
40	28	35.4	8	14	US-10-008-524A-26
41	28	35.4	8	14	US-10-008-524A-27
42	28	35.4	8	14	US-10-008-524A-28
43	28	35.4	8	14	US-10-008-524A-29
44	28	35.4	8	15	US-10-350-719-26
45	28	35.4	8	15	US-10-350-719-27

ALIGNMENTS

RESULT 1

US-09-938-315-92
Sequence 92, Application US/09938315
Patent No. US20020091085A1
GENERAL INFORMATION:
APPLICANT: KAY, BRIAN K.
SPARKS, ANDREW B.
THORN, JUDITH M.
QUILLIAM, LAWRENCE A.
DER, CHANNING J.
TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT, P.C.
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
STREET: 1755 S. Jefferson Davis Highway, Suite 400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,315
FILING DATE: 23-Aug-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-007-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 92:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 92:
 US-09-938-315-92

Query Match 44.3%; Score 35; DB 9; Length 13;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SPRPLPV 15
 Db 2 TPRPLPI 9

RESULT 2
 US-10-161-791-92
 ; Sequence 92, Application US/10161791
 ; Publication No. US20030186863A1

; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: THORN, Judith M.
 ; APPLICANT: QUILLIAM, Lawrence A.
 ; APPLICANT: DER, Channing J.
 ; APPLICANT: FOWLKES, Dana M.
 ; APPLICANT: RIDER, James E.
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 ; TITLE OF INVENTION: ISOLATING AND USING SAME
 ; NUMBER OF SEQUENCES: 467
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/161,791

; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/602,999
 ; FILING DATE: 16-FEB-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 1101-202
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 92:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide

US-10-161-791-92

Query Match 44.3%; Score 35; DB 14; Length 13;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SPRPLPV 15

Db :|||||: 2 TPRPLPI 9

RESULT 3

US-09-945-917-17
 ; Sequence 17, Application US/09945917
 ; Publication No. US20030042381A1

; GENERAL INFORMATION:
 ; APPLICANT: Bogaert, Thierry
 ; APPLICANT: Vandekerckhove, Joel
 ; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
 ; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
 ; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
 ; FILE REFERENCE: P/14-1
 ; CURRENT APPLICATION NUMBER: US/09/945,917
 ; CURRENT FILING DATE: 1998-09-21
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 17
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-09-945-917-17

Query Match 43.0%; Score 34; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PRPLPV 14
 Db 2 PRPLPV 7

RESULT 4

US-09-845-917A-17
 ; Sequence 17, Application US/09845917A
 ; Publication No. US20030167538A1

; GENERAL INFORMATION:
 ; APPLICANT: Bogaert, Thierry
 ; APPLICANT: Vandekerckhove, Joel
 ; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
 ; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
 ; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
 ; FILE REFERENCE: P/14-1
 ; CURRENT APPLICATION NUMBER: US/09/845,917A
 ; CURRENT FILING DATE: 2001-04-30
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 17
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-09-845-917A-17

Query Match 43.0%; Score 34; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PRPLPV 14
 Db 2 PRPLPV 7

RESULT 5

US-10-161-791-255
 ; Sequence 255, Application US/10161791
 ; Publication No. US20030186863A1

; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: KAY, Brian K.

APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 255:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-255

Query Match 43.0%; Score 34; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
|||||
Db 3 PRPLPV 8

RESULT 6
US-10-161-791-410
Sequence 410, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 410:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-410

Query Match 43.0%; Score 34; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
|||||
Db 4 PRPLPV 9

RESULT 7
US-09-938-315-86
Sequence 86, Application US/09938315
Patent No. US20020091085A1
GENERAL INFORMATION:
APPLICANT: KAY, BRIAN K.
SPARKS, ANDREW B.
THORN, JUDITH M.
QUILLIAM, LAWRENCE A.
DER, CHANNING J.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,315
FILING DATE: 23-Aug-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-007-0
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-938-315-86

Query Match 41.8%; Score 33; DB 9; Length 13;
Best Local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SPRPLPVV 15
Db 2 TPRPLPWL 9

RESULT 8
US-10-161-791-86
; Sequence 86, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-86

Query Match 41.8%; Score 33; DB 14; Length 13;
Best Local Similarity 62.5%; Pred. No. 2.2e+02;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 8 SPRPLPVV 15
Db 2 TPRPLPWL 9

RESULT 9
US-09-938-315-62
; Sequence 62, Application US/09938315
; Patent No. US20020091085A1
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; SPARKS, ANDREW B.
; THORN, JUDITH M.
; QUILLIAM, LAWRENCE A.
; DER, CHANNING J.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,315
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <UNKNOWN>
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-09-938-315-62

Query Match 41.8%; Score 33; DB 9; Length 14;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SPRPLPVV 15
Db 3 TPRPLPWL 10

RESULT 10
US-10-161-791-62
; Sequence 62, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.

APPLICANT: FOWLKES, Dana M.
 APPLICANT: RIDER, James E.
 TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 TITLE OF INVENTION: ISOLATING AND USING SAME
 NUMBER OF SEQUENCES: 467
 CORRESPONDENCE ADDRESS:
 ADDRESS: Pennie & Edmonds
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/161,791
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/602,999
 FILING DATE: 16-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 1101-202
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 62:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-10-161-791-62

Query Match 41.8%; Score 33; DB 14; Length 14;
 Best Local Similarity 62.5%; Pred. No. 2.4e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLPV 15
 DB 3 TPRPLML 10

RESULT 11
 US-09-938-315-67
 Sequence 67, Application US/09938315
 Patent No. US20020091085A1
 GENERAL INFORMATION:
 APPLICANT: KAY, BRIAN K.
 APPLICANT: SPARKS, ANDREW B.
 APPLICANT: THORN, JUDITH M.
 APPLICANT: QUILLIAM, LAWRENCE A.
 APPLICANT: DER, CHANNING J.
 TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF
 ISOLATING AND USING SAME
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESS: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
 STREET: 1755 S. Jefferson Davis Highway, Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/938,315
 FILING DATE: 23-Aug-2001
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Villacorta, Gilberto M.
 REGISTRATION NUMBER: 34,038
 REFERENCE/DOCKET NUMBER: 4980-007-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220
 TELEX: 248955 OPAT UR
 INFORMATION FOR SEQ ID NO: 67:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 67:
 US-09-938-315-67
 Query Match 39.2%; Score 31; DB 9; Length 14;
 Best Local Similarity 83.3%; Pred. No. 4.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLP 13
 DB 3 TPRPLP 8

RESULT 12
 US-10-161-791-67
 Sequence 67, Application US/10161791
 Publication No. US2003018683A1
 GENERAL INFORMATION:
 APPLICANT: SPARKS, Andrew B.
 APPLICANT: KAY, Brian K.
 APPLICANT: THORN, Judith M.
 APPLICANT: QUILLIAM, Lawrence A.
 APPLICANT: DER, Channing J.
 APPLICANT: FOWLKES, Dana M.
 APPLICANT: RIDER, James E.
 TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
 TITLE OF INVENTION: ISOLATING AND USING SAME
 NUMBER OF SEQUENCES: 467
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/161,791
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/602,999
 FILING DATE: 16-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 1101-202
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-67

Query Match 39.2%; Score 31; DB 14; Length 14;
Best Local Similarity 83.3%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SPRPLP 13
Db 3 TPRPLP 8

RESULT 13

US-09-815-837-114
; Sequence 114, Application US/09815837
; Patent No. US20020082411A1

; GENERAL INFORMATION:

; APPLICANT: Carter, Darrick
; APPLICANT: Zhu, Shirley
; APPLICANT: Arimilli, Subhashini
; APPLICANT: Wang, Aijun
; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Immune Mediators and Related Methods

; FILE REFERENCE: 014058-005670US

; CURRENT APPLICATION NUMBER: US/09/815,837

; CURRENT FILING DATE: 2001-03-22

; PRIOR APPLICATION NUMBER: US 60/191,274

; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: US 60/204,249

; PRIOR FILING DATE: 2000-05-15

; PRIOR APPLICATION NUMBER: US 60/264,003

; PRIOR FILING DATE: 2001-01-23

; NUMBER OF SEQ ID NOS: 129

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 114

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:downstream

; OTHER INFORMATION: linker for COS85 and COS92

US-09-815-837-114

Query Match 38.0%; Score 30; DB 9; Length 8;
Best Local Similarity 62.5%; Pred. No. 9.7e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FGSPRPLP 13
Db 1 FDAPSPLP 8

RESULT 14

US-10-149-138-4631

; Sequence 4631, Application US/10149138

; Publication No. US20040018971A1

; GENERAL INFORMATION:

; APPLICANT: Fikes, John

; APPLICANT: Sette, Alessandro

; APPLICANT: Sidney, John

; APPLICANT: Southwood, Scott

; APPLICANT: Cheenut, Robert

; APPLICANT: Celis, Esteban

; APPLICANT: Keogh, Elissa

; TITLE OF INVENTION: Inducing Cellular Immune Responses to

; FILE REFERENCE: HER2/neu Using Peptide and Nucleic Acid Compositions

; FILE REFERENCE: 2060.0140001

; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4631
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4631

Query Match 38.0%; Score 30; DB 15; Length 11;
Best Local Similarity 63.6%; Pred. No. 5.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

Qy 6 FGSPR--PLPV 14
Db 1 FPSPREGLPI 11

RESULT 15

US-10-286-457-30

; Sequence 30, Application US/10286457

; Publication No. US20030166004A1

; GENERAL INFORMATION:

; APPLICANT: JENO GYURIS et al.

; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY

; FILE REFERENCE: GPCI-P01-178

; CURRENT APPLICATION NUMBER: US/10/286,457

; CURRENT FILING DATE: 2002-11-01

; PRIOR APPLICATION NUMBER: 60/334822

; PRIOR FILING DATE: 2001-11-01

; NUMBER OF SEQ ID NOS: 684

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 30

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based on ability to selectively bind to endothelial cells

; OTHER INFORMATION: ability to selectively bind to endothelial cells

US-10-286-457-30

Query Match 38.0%; Score 30; DB 14; Length 12;
Best Local Similarity 60.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 HSGSPRPLP 13
Db 2 HKPSPPTPLP 11

Search completed: April 2, 2004, 10:23:35
Job time : 32.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 09:56:18 ; Search time 46 Seconds
(without alignments)
92.135 Million cell updates/sec

Title: US-10-009-049-3

Perfect score: 82

Sequence: 1 CRAHSFVSRLPVV 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1596107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 447529

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	100.0	15	4	AAB59251 Peptide #
2	75	91.5	15	4	AAB59249 Peptide r
3	66	80.5	15	4	AAB59250 Peptide #
4	39	47.6	15	2	AAB05069 Proline-r
5	37	45.1	10	4	AAB06985
6	37	45.1	10	4	AAM08985 CYP1B1 HL
7	37	45.1	10	4	AAM12950 HLA-A*02
8	37	45.1	10	4	AAM08833 HLA-A1 de
9	37	45.1	10	4	AAM09489 HLA-B*07
10	35	42.7	13	2	AAM11111 Src SH3 d
11	35	42.7	13	2	AAM05098 Proline-r
12	34	41.5	9	2	AAM094619 Src homol
13	34	41.5	10	4	AAM09403
14	34	41.5	10	4	AAM13226 HLA-A26 d
15	34	41.5	10	4	AAM11873 HLA-A*02
16	34	41.5	10	4	AAM09177 HLA-A*02
17	34	41.5	10	4	AAM09490 HLA-B*07
18	34	41.5	12	2	AAM16127 Peptide c
19	34	41.5	12	2	AAM68767 Peptide b
20	34	41.5	12	2	AAM58254 Interleuk
21	34	41.5	12	2	AAY09898 Interleuk
22	34	41.5	12	2	AB17679 IL-1 anta
23	34	41.5	12	5	ABB72575 Interleuk
24	34	41.5	15	2	AAM39011 Peptide r
25	33	40.2	9	4	AAM11755 HLA-B*15

26	33	40.2	9	4	AAM07477
27	33	40.2	9	4	AAM07008
28	33	40.2	9	4	AAM06907 Cytochrom
29	33	40.2	9	4	AAM08918 HLA-B*27
30	33	40.2	9	4	AAM06958 CYP1B1 HL
31	33	40.2	9	4	AAM11125 HLA-B8 no
32	33	40.2	9	4	AAM11262 HLA-A26 n
33	33	40.2	9	4	AAM07025 HLA-A1 no
34	33	40.2	9	4	AAM06929 HLA-A2 pr
35	33	40.2	9	5	ABG68876 Human CYP
36	33	40.2	13	2	AAM11105 Src SH3 d
37	33	40.2	14	2	AAR93450 GST-PI3K
38	33	40.2	14	2	AAR93395 GST-PYV S
39	33	40.2	14	2	AAM11098 Src SH3 d
40	33	40.2	14	2	AAM25512 SH3 synth
41	33	40.2	14	4	AAM53295 Human non
42	32	39.0	14	1	AAP60604 Sequence
43	31	37.8	8	4	AAM09704 HLA-B8 oc
44	31	37.8	9	4	AAM08460 HLA-B*27
45	31	37.8	9	4	AAM12347 HLA-A*02

ALIGNMENTS

RESULT 1
AAB59251
ID AAB59251 standard; peptide; 15 AA.
XX AC AAB59251;
XX DT 27-MAR-2001 (first entry)
XX DE Peptide #3 recognised by gene VIII library clone 45.
XX KW Fibrin fragment E; cell proliferation; cancer; vascular restenosis;
XX KW arthritis; diabetes; renal disease; psoriasis.
XX OS Synthetic.
XX PN WO200075175-A1.
XX PD 14-DEC-2000.
XX PF 07-JUN-2000; 2000WO-GB002197.
XX PR 07-JUN-1999; 99GB-00012994.
XX (UYAB-) UNIV ABERDEEN.
XX Melvin WT, Thompson WD, Stirk CM;
XX WPI; 2001-080581/09.
XX New peptides capable of modulating a fibrin fragment E activity, useful
XX for inhibiting uncontrolled cell proliferation, e.g. for treating cancer,
XX vascular restenosis, atherogenesis or psoriasis, and for wound healing.
XX Claim 1; Page 49; 59pp; English.

The present invention relates to a peptide or its fragment, which is capable of modulating a fibrin fragment E activity. The peptides and modulators are useful for inhibiting stimulation of cell proliferation induced by a fibrin degradation product. The antibody or binding fragment is also useful for identifying the active site of the fibrin fragment E receptor. The peptides are particularly useful in treating cancer, vascular restenosis, rheumatoid arthritis, diabetes, renal diseases or psoriasis. The antibodies are also useful for modulating the activity of the peptide

Sequence 15 AA;

Query Match 100.0%; Score 82; DB 4; Length 15;

XX	Fibrin fragment E; cell proliferation; cancer; vascular restenosis; arthritis; diabetes; renal disease; psoriasis.
KW	Synthetic.
OS	WO200075175-A1.
XX	14-DEC-2000.
PN	07-JUN-2000; 2000WO-GB002197.
XX	07-JUN-1999; 99GB-00012994.
XX	(UYAB-) UNIV ABERDEEN.
XX	Melvin WT, Thompson WD, Stirk CM;
XX	WPI; 2001-080581/09.
XX	New peptides capable of modulating a fibrin fragment E activity, useful for inhibiting uncontrolled cell proliferation, e.g. for treating cancer, vascular restenosis, atherogenesis or psoriasis, and for wound healing.
PT	Claim 1; Page 49; 59pp; English.
XX	The present invention relates to a peptide or its fragment, which is capable of modulating a fibrin fragment E activity. The peptides and modulators are useful for inhibiting stimulation of cell proliferation induced by a fibrin degradation product. The antibody or binding fragment is also useful for identifying the active site of the fibrin fragment E receptor. The peptides are particularly useful in treating cancer, vascular restenosis, rheumatoid arthritis, diabetes, renal diseases or psoriasis. The antibodies are also useful for modulating the activity of the peptide
CC	Sequence 15 AA;
XX	Query Match 80.5%; Score 66; DB 4; Length 15;
SQ	Best Local Similarity 92.9%; Pred. No. 0.00057;
	Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	2 RAHSFVSPRPPLPVV 15
Db	2 RAHSFGSPRPPLPVV 15
	RESULT 4
AAW05069	ID AAW05069 standard; peptide; 15 AA.
XX	AAW05069;
XX	25-MAR-2003 (revised)
DT	17-DEC-1996 (first entry)
XX	Proline-rich SH3 binding peptide fuse5B-4.51 from random library.
DE	Src homology domain; SH3 domain; oncogene; consensus; random display library.
XX	Synthetic.
XX	Key Location/Qualifiers
FF	Region 7..13
FT	/label= SH3 binding motif
FT	/note= "corresponds to consensus sequence RPLPXXP"
XX	USS541109-A.
XX	30-JUL-1996.
XX	19-APR-1994; 94US-00230047.

XX 19-APR-1994; 94US-00230047.
 XX (RHON) RHONE POULENC RORER PHARM INC.
 XX Ivashchenko YD, Ricca GA, Cheadle C, South VJ, Jaye MC;
 XX French SM, Searfoss GH;
 XX WPI; 1996-361965/36.
 XX New DNA encoding proteins that bind to Src-homology domain 3 - used to
 XX inhibit signal transduction, e.g. in cases of T cell activation.
 XX Example 1; Col 7; 39pp; English.
 XX A fusion phage library for expressing random 15mer peptides was prepared
 XX using the filamentous bacteriophage fuse 5B. The display library was
 XX screened for peptides which bind to the Src SH3 domain. A sequence
 XX comparison of the positive peptides revealed a highly reiterated, proline
 XX rich, 7 amino acid consensus motif (i.e. the sequence RPLPXP). This
 XX motif demonstrated a strong similarity to a Src SH3 binding sequence
 XX identified within a protein isolated by screening a lambda-lox mouse
 XX embryo cDNA library with a Src SH3 domain probe. The present sequence is
 XX that of one of the positive peptides identified from the fuse 5B random
 XX display library. (Updated on 25-MAR-2003 to correct PI field.)
 XX SQ Sequence 15 AA;

Query Match 47.6%; Score 39; DB 2; Length 15;
 Best Local Similarity 70.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 HSFVSPRPLP 13
 | | | | |
 Db 1 HSHFPRPLP 10

RESULT 5
 AAM06985
 ID AAM06985 standard; peptide; 10 AA.
 XX AC AAM06985;
 XX 09-OCT-2001 (first entry)
 XX CYP1B1 HLA-A2 binding peptide fragment #35.
 XX Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA;
 XX human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; APC;
 XX major histocompatibility complex; antigen presenting cell; melanoma;
 XX lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.
 XX Homo sapiens.
 XX WO200135810-A2.
 XX 25-MAY-2001.
 XX 15-NOV-2000; 2000WO-US031513.
 XX 15-NOV-1999; 99US-0165590P.
 XX (DAND) DANA FARBBER CANCER INST INC.
 XX (UYBO-) UNIV BOSTON.
 XX Schultze JL, Vonderheide RH, Sherr D, Nadler LM, Maecker B;
 XX Von Bergwelt- Baildon M;
 XX WPI; 2001-355537/37.
 XX Treating a cancer patient involves administering to patient a cytotoxic T
 XX -lymphocyte, an antigen presenting cell that activates T cells, a peptide
 XX of cytochrome P450 1B1, or a polynucleotide encoding the peptide.

XX PS Disclosure; Page 40; 121pp; English.
 XX The present invention describes a method for treating a patient having,
 XX or is at risk of having, a cell expressing cytochrome P450 1B1 (CYP1B1),
 XX which involves administering to the patient a cytotoxic T-lymphocyte
 XX (CTL) that kills the cell, an antigen presenting cell (APC) that
 XX activates CTL, a peptide of CYP1B1 that binds to major histocompatibility
 XX complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or
 XX peptide of CYP1B1. Also described are: (1) a method for assessing the
 XX level of immunity of a patient to CYP1B1 or a peptide of CYP1B1 that
 XX binds to MHC complex molecule, involving measuring the level of CTL
 XX specific for CYP1B1 or the peptide of CYP1B1 in a sample from the patient
 XX; (2) a CYP1B1 peptide (I) that binds to MHC complex molecule; (3) an ex
 XX vivo generated CTL (II) that specifically kills a cell expressing CYP1B1
 XX in a specific of a MHC complex-restricted fashion; and (4) an ex vivo
 XX generated APC (III) that presents a peptide of a CYP1B1 in the context of
 XX a MHC complex molecule. The method is useful for treating a patient
 XX having or is at risk of having a cell that expresses CYP1B1. The method
 XX is useful for the prevention, treatment and diagnosis of cancer, e.g.
 XX melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and
 XX lung, ovarian, uterine, cervical, prostate, liver, colon, pancreatic and
 XX brain cancer. AAM06905 to AAM13566 represent CYP1B1 peptides which can
 XX bind to human leukocyte antigens (HLAs), as well as other amino acid
 XX sequence used in the exemplification of the present invention
 XX SQ Sequence 10 AA;

Query Match 45.1%; Score 37; DB 4; Length 10;
 Best Local Similarity 70.0%; Pred. No. 23;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 FVSPRPLPVV 15
 | : | | | | |
 Db 1 FLDFRPLTVV 10

RESULT 6
 AAM08985
 ID AAM08985 standard; peptide; 10 AA.
 XX AC AAM08985;
 XX 09-OCT-2001 (first entry)
 XX HLA-A *0201 decamer #2.
 XX Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA;
 XX human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; APC;
 XX major histocompatibility complex; antigen presenting cell; melanoma;
 XX lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.
 XX Homo sapiens.
 XX WO200135810-A2.
 XX 25-MAY-2001.
 XX 15-NOV-2000; 2000WO-US031513.
 XX 15-NOV-1999; 99US-0165590P.
 XX (DAND) DANA FARBBER CANCER INST INC.
 XX (UYBO-) UNIV BOSTON.
 XX Schultze JL, Vonderheide RH, Sherr D, Nadler LM, Maecker B;
 XX Von Bergwelt- Baildon M;
 XX WPI; 2001-355537/37.
 XX Treating a cancer patient involves administering to patient a cytotoxic T
 XX -lymphocyte, an antigen presenting cell that activates T cells, a peptide
 XX of cytochrome P450 1B1, or a polynucleotide encoding the peptide.

XX Disclosure; Page 69; 121pp; English.

XX The present invention describes a method for treating a patient having,

XX or is at risk of having, a cell expressing cytochrome P450 1B1 (CYP1B1),

XX which involves administering to the patient a cytotoxic T-lymphocyte

XX (CTL) that kills the cell, an antigen presenting cell (APC) that

XX activates CTL, a peptide of CYP1B1 that binds to major histocompatibility

XX complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or

XX peptide of CYP1B1. Also described are: (1) a method for assessing the

XX level of immunity of a patient to CYP1B1 or a peptide of CYP1B1 that

XX binds to MHC complex molecule, involving measuring the level of CTL

XX specific for CYP1B1 or the peptide of CYP1B1 in a sample from the patient

XX; (2) a CYP1B1 peptide (I) that binds to MHC complex molecule; (3) an ex

XX vivo generated CTL (II) that specifically kills a cell expressing CYP1B1

XX in a specific of a MHC complex-restricted fashion; and (4) an ex vivo

XX generated APC (III) that presents a peptide of a CYP1B1 in the context of

XX a MHC complex molecule. The method is useful for treating a patient

XX having or is at risk of having a cell that expresses CYP1B1. The method

XX is useful for the prevention, treatment and diagnosis of cancer, e.g.

XX melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and

XX lung, ovarian, uterine, cervical, prostate, liver, colon, pancreatic and

XX brain cancer. AAM06905 to AAM13566 represent CYP1B1 peptides which can

XX bind to human leukocyte antigens (HLAs), as well as other amino acid

XX sequence used in the exemplification of the present invention

SQ Sequence 10 AA;

Query Match 45.1%; Score 37; DB 4; Length 10;
 Best Local Similarity 70.0%; Pred. No. 23;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 FVSRRPLPVW 15
 | : | | | | | |
 Db 1 FLDRPLTVW 10

RESULT 7
 AAM12950
 ID AAM12950 standard; peptide; 10 AA.
 XX
 AC AAM12950;
 XX
 DT 09-OCT-2001 (first entry)
 XX
 DE HLA-A26 decamer #87.
 XX
 KW Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA;
 KW human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; APC;
 KW major histocompatibility complex; antigen presenting cell; melanoma;
 KW lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 FN WO200135810-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 15-NOV-2000; 2000WO-US031513.
 XX
 PR 15-NOV-1999; 99US-0165590P.
 XX
 XX (DAND) DANA FARBER CANCER INST INC.
 PA (UYBO-) UNIV BOSTON.
 XX
 PI Schultze JL, Vonderheide RH, Sherr D, Nadler LM, Maecker B;
 PI Von Bergwelt- Baildon M;
 XX
 DR WPI; 2001-355537/37.

PT Treating a cancer patient involves administering to patient a cytotoxic T

PT -lymphocyte, an antigen presenting cell that activates T cells, a peptide

PT of cytochrome P450 1B1, or a polynucleotide encoding the peptide.

XX Disclosure; Page 89; 121pp; English.

XX The present invention describes a method for treating a patient having,

XX or is at risk of having, a cell expressing cytochrome P450 1B1 (CYP1B1),

XX which involves administering to the patient a cytotoxic T-lymphocyte

XX (CTL) that kills the cell, an antigen presenting cell (APC) that

XX activates CTL, a peptide of CYP1B1 that binds to major histocompatibility

XX complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or

XX peptide of CYP1B1. Also described are: (1) a method for assessing the

XX level of immunity of a patient to CYP1B1 or a peptide of CYP1B1 that

XX binds to MHC complex molecule, involving measuring the level of CTL

XX specific for CYP1B1 or the peptide of CYP1B1 in a sample from the patient

XX; (2) a CYP1B1 peptide (I) that binds to MHC complex molecule; (3) an ex

XX vivo generated CTL (II) that specifically kills a cell expressing CYP1B1

XX in a specific of a MHC complex-restricted fashion; and (4) an ex vivo

XX generated APC (III) that presents a peptide of a CYP1B1 in the context of

XX a MHC complex molecule. The method is useful for treating a patient

XX having or is at risk of having a cell that expresses CYP1B1. The method

XX is useful for the prevention, treatment and diagnosis of cancer, e.g.

XX melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and

XX lung, ovarian, uterine, cervical, prostate, liver, colon, pancreatic and

XX brain cancer. AAM06905 to AAM13566 represent CYP1B1 peptides which can

XX bind to human leukocyte antigens (HLAs), as well as other amino acid

XX sequence used in the exemplification of the present invention

SQ Sequence 10 AA;

Query Match 45.1%; Score 37; DB 4; Length 10;
 Best Local Similarity 70.0%; Pred. No. 23;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 FVSRRPLPVW 15
 | : | | | | | |
 Db 1 FLDRPLTVW 10

RESULT 8
 AAM08833
 ID AAM08833 standard; peptide; 10 AA.
 XX
 AC AAM08833;
 XX
 DT 09-OCT-2001 (first entry)
 XX
 DE HLA-A1 decamer #12.
 XX
 KW Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA;
 KW human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; APC;
 KW major histocompatibility complex; antigen presenting cell; melanoma;
 KW lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 FN WO200135810-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 15-NOV-2000; 2000WO-US031513.
 XX
 PR 15-NOV-1999; 99US-0165590P.
 XX
 XX (DAND) DANA FARBER CANCER INST INC.
 PA (UYBO-) UNIV BOSTON.
 XX
 PI Schultze JL, Vonderheide RH, Sherr D, Nadler LM, Maecker B;
 PI Von Bergwelt- Baildon M;
 XX
 DR WPI; 2001-355537/37.

PT Treating a cancer patient involves administering to patient a cytotoxic T

PT -lymphocyte, an antigen presenting cell that activates T cells, a peptide

PT of cytochrome P450 1B1, or a polynucleotide encoding the peptide.

XX Disclosure; Page 68; 121pp; English.

CC The present invention describes a method for treating a patient having, or is at risk of having, a cell expressing cytochrome P450 1B1 (CYP1B1), which involves administering to the patient a cytotoxic T-lymphocyte (CTL) that kills the cell, an antigen presenting cell (APC) that activates CTL, a peptide of CYP1B1 that binds to major histocompatibility complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or peptide of CYP1B1. Also described are: (1) a method for assessing the level of immunity of a patient to CYP1B1 or a peptide of CYP1B1 that binds to MHC complex molecule, involving measuring the level of CTL specific for CYP1B1 or the peptide of CYP1B1 in a sample from the patient; (2) a CYP1B1 peptide (I) that binds to MHC complex molecule; (3) an ex vivo generated CTL (II) that specifically kills a cell expressing CYP1B1 in a specific of a MHC complex-restricted fashion; and (4) an ex vivo generated APC (III) that presents a peptide of a CYP1B1 in the context of a MHC complex molecule. The method is useful for treating a patient having or is at risk of having a cell that expresses CYP1B1. The method is useful for the prevention, treatment and diagnosis of cancer, e.g. melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and lung, ovarian, uterine, cervical, prostate, liver, colon, pancreatic and brain cancer. AAM06905 to AAM13566 represent CYP1B1 peptides which can bind to human leukocyte antigens (HLAs), as well as other amino acid sequence used in the exemplification of the present invention

XX Sequence 10 AA;

QY 6 FVSPRPPLPVV 15
| : ||||| ||
DB 1 FLDPRLPTVV 10

RESULT 9
AAM09489
ID AAM09489 standard; peptide; 10 AA.
XX AC AAM09489;
DT 09-OCT-2001 (first entry)
XX HLA-B *0702 decamer #115.
XX Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA; human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; APC; major histocompatibility complex; antigen presenting cell; melanoma; lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.
XX Homo sapiens.
XX WO200135810-A2.
XX 25-MAY-2001.
XX 15-NOV-2000; 2000WO-US031513.
XX 15-NOV-1999; 99US-0165590P.
XX (DAND) DANA FARBER CANCER INST INC.
XX (UYBO-) UNIV BOSTON.
XX Schultze JL, Vonderheide RH, Sherr D, Nadler LM, Maecker B; Von Bergwelt- Baildon M;
XX WPI; 2001-355537/37.
XX Treating a cancer patient involves administering to patient a cytotoxic T-lymphocyte, an antigen presenting cell that activates T cells, a peptide of cytochrome P450 1B1, or a polynucleotide encoding the peptide.

XX Disclosure; Page 71; 121pp; English.

CC The present invention describes a method for treating a patient having, or is at risk of having, a cell expressing cytochrome P450 1B1 (CYP1B1), which involves administering to the patient a cytotoxic T-lymphocyte (CTL) that kills the cell, an antigen presenting cell (APC) that activates CTL, a peptide of CYP1B1 that binds to major histocompatibility complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or peptide of CYP1B1. Also described are: (1) a method for assessing the level of immunity of a patient to CYP1B1 or a peptide of CYP1B1 that binds to MHC complex molecule, involving measuring the level of CTL specific for CYP1B1 or the peptide of CYP1B1 in a sample from the patient; (2) a CYP1B1 peptide (I) that binds to MHC complex molecule; (3) an ex vivo generated CTL (II) that specifically kills a cell expressing CYP1B1 in a specific of a MHC complex-restricted fashion; and (4) an ex vivo generated APC (III) that presents a peptide of a CYP1B1 in the context of a MHC complex molecule. The method is useful for treating a patient having or is at risk of having a cell that expresses CYP1B1. The method is useful for the prevention, treatment and diagnosis of cancer, e.g. melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and lung, ovarian, uterine, cervical, prostate, liver, colon, pancreatic and brain cancer. AAM06905 to AAM13566 represent CYP1B1 peptides which can bind to human leukocyte antigens (HLAs), as well as other amino acid sequence used in the exemplification of the present invention

XX Sequence 10 AA;

QY 6 FVSPRPPLPVV 15
| : ||||| ||
DB 1 FLDPRLPTVV 10

RESULT 10
AAW11111
ID AAW11111 standard; peptide; 13 AA.
XX AC AAW11111;
DT 25-JUN-1997 (first entry)
XX Src SH3 domain-binding peptide used in signal transduction modulation.
XX Src; SH3; Src homology region 3; binding affinity; oncogenic protein; protein tyrosine kinase; signal transduction; RNA processing; trafficking; translation.
XX Synthetic.
XX WO9603649-A1.
XX 08-FEB-1996.
XX 24-JUL-1995; 95WO-US009382.
XX 22-JUL-1994; 94US-00278865.
XX 07-JUN-1995; 95US-00483555.
XX (UYNC-) UNIV NORTH CAROLINA.
XX Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CJ;
XX WPI; 1996-117151/12.
XX Peptide with binding affinity for Src homology region 3 (SH3) domains of proteins - useful for e.g. modulating signal transduction pathways at the cellular level, esp. protein tyrosine kinase-mediated.
XX Claim 38; Page 87; 116pp; English.

XX AAW11098-W1124 are peptides that bind to the Src SH3 domain. The SH3
 CC binding peptides are useful in modulating signal transduction pathways at
 CC the cellular level (especially protein tyrosine kinase-mediated),
 CC modulating oncogenic protein activity, or providing compounds for the
 CC development of drugs with the ability to modulate broad classes, as well
 CC as specific classes, of proteins involved in signal transduction and also
 CC for regulating the processing, trafficking or translation of RNA.
 CC Conjugates of the peptides with detectable labels or imaging agents are
 CC useful for imaging cells, tissues and organs in which Src or Src-related
 CC proteins are expressed
 XX Sequence 13 AA;
 SQ

Query Match 42.7%; Score 35; DB 2; Length 13;
 Best Local Similarity 62.5%; Pred. No. 65;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLFW 15
 Db 2 TTRPLPI 9
 :|||||:

RESULT 11
 AAW05098
 ID AAW05098 standard; peptide; 13 AA.
 XX
 AC AAW05098;
 XX
 XX 25-MAR-2003 (revised)
 DT 17-DEC-1996 (first entry)
 XX
 DE Proline-rich SH3 binding peptide L14-2.
 XX
 XX Src homology domain; SH3 domain; oncogene; consensus; lambda 14;
 KW random display library.
 XX
 XX Synthetic.
 XX
 XX US5541109-A.
 XX
 XX 30-JUL-1996.
 XX
 XX 19-APR-1994; 94US-00230047.
 XX
 XX 19-APR-1994; 94US-00230047.
 XX
 XX (RHON) RHONE POULENC RORER PHARM INC.
 XX
 XX Ivaashchenko YD, Ricca GA, Cheadle C, South VU, Jaye MC;
 PI French SM, Searfoss GH;
 XX
 XX WPI; 1996-361965/36.
 XX
 XX New DNA encoding proteins that bind to Src-homology domain 3 - used to
 PT inhibit signal transduction, e.g. in cases of T cell activation.
 XX
 XX Example 1; Col 16; 39pp; English.
 XX

CC A fusion protein of glutathione-S-transferase, protein kinase A and Src
 CC SH3 domain was used to screen a mouse embryonal cDNA library in lambda
 CC Exlox. Three positive clones were identified and were designated L17, L14
 CC and L35. The insert from clone L14 contains a 221 bp region with
 CC approximately 90% identity to an anonymous cDNA (EST06380) directionally
 CC cloned from a human infant brain cDNA library. The deduced amino acid
 CC sequence contains two proline-rich, putative SH3-binding sequences. The
 CC present peptide sequence is derived from the putative SH3-binding site at
 CC residues 241-253 of L14 and was used in an assay to determine binding to
 CC the SH3 domains of c-src and other proteins. (Updated on 25-MAR-2003 to
 CC correct PI field.)
 XX
 XX Sequence 13 AA;
 SQ

Query Match 42.7%; Score 35; DB 2; Length 13;
 Best Local Similarity 70.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 HSFVSPRLP 13
 Db 3 HSAVPRPGP 12
 :|||||:

RESULT 12
 AAW94619
 ID AAW94619 standard; peptide; 9 AA.
 XX
 XX AAW94619;
 XX
 XX 29-APR-1999 (first entry)
 DT
 XX
 DE Src homology 3 domain binding nonamer peptide #1.
 XX
 XX Src homology 3 domain; SH3 domain; peptidomimetic; mimetic; modulator;
 KW beta-turn template; spiro[pyrrolidine-2':3-piperidin-2-ones];
 KW fused ring analogue; signal transduction protein interaction;
 KW inhibit cell growth; infection; cancer.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "acetylated"
 XX
 XX W09854208-A1.
 XX
 XX 03-DEC-1998.
 XX
 XX 28-MAY-1998; 98WO-US010861.
 XX
 XX 28-MAY-1997; 97US-00864241.
 PR 18-MAY-1998; 98US-0085889P.
 XX
 XX (CADU-) CADUS PHARM CORP.
 XX
 XX Castelhamo AL, Witter DJ;
 PI
 XX WPI; 1999-080804/07.
 XX
 XX spiro[pyrrolidine-2':3-piperidin-2-ones] and their fused ring analogues -
 PT used, e.g. to modulate signal transduction protein interactions, inhibit
 PT cell growth and for use in treating infections and cancer.
 XX
 XX Example 12; Page 59; 73pp; English.
 XX

CC The present invention describes spiro[pyrrolidine-2':3-piperidin-2-ones],
 CC their fused ring analogues, and salts of both, all as individual
 CC compounds or their libraries. They are peptidomimetics, and interact with
 CC protein Src homology 3 (SH3) domains, involved in protein-protein
 CC interactions in signal transduction. They cause disruption of the pathway
 CC in particular, they inhibit the protein tyrosine kinase system involved
 CC in cell growth regulation. The cells may be microbial, e.g. pathogenic
 CC bacterial or fungal cells responsible for infections, or of transformed
 CC cells, e.g. responsible for neoplastic conditions. Specific examples of
 CC Src proteins with SH3 domains are those known by the abbreviations p85,
 CC Fyn, Lyn, Hck, Syk, Grb2, Gap, STAT, p47-phox, p67-phox, and Bcr. The
 CC present sequence represents a nonamer peptide used in an example from the
 CC present invention
 XX
 XX Sequence 9 AA;
 SQ

Query Match 41.5%; Score 34; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
 :|||||:

Db 1 PRELPV 6

RESULT 13

AA09403

ID AAM09403 standard; peptide; 10 AA.

XX AC AAM09403;

XX DT 09-OCT-2001 (first entry)

XX DE HLA-A1 decamer #122.

XX KW Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA;

XX KW human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; APC;

XX KW major histocompatibility complex; antigen presenting cell; melanoma;

XX KW lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.

XX OS Homo sapiens.

XX PN WO200135810-A2.

XX PD 25-MAY-2001.

XX PF 15-NOV-2000; 2000WO-US031513.

XX PR 15-NOV-1999; 99US-0165590P.

XX PA (DAND) DANA FARBER CANCER INST INC.

XX PA (UYBO-) UNIV BOSTON.

XX PI Schultze JL, Vonderheide RH, Sherr D, Nadler LM, Maecker B;

XX PI Von Bergwelt- Balldon M;

XX DR WPI; 2001-355537/37.

XX PT Treating a cancer patient involves administering to patient a cytotoxic T

XX PT -lymphocyte, an antigen presenting cell that activates T cells, a peptide

XX PT of cytochrome P450 1B1, or a polynucleotide encoding the peptide.

XX PS Disclosure; Page 71; 121pp; English.

XX CC The present invention describes a method for treating a patient having,

XX CC or is at risk of having, a cell expressing cytochrome P450 1B1 (CYP1B1),

XX CC which involves administering to the patient a cytotoxic T-lymphocyte

XX CC (CTL) that kills the cell, an antigen presenting cell (APC) that

XX CC activates CTL, a peptide of CYP1B1 that binds to major histocompatibility

XX CC complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or

XX CC peptide of CYP1B1. Also described are: (1) a method for assessing the

XX CC level of immunity of a patient to CYP1B1 or a peptide of CYP1B1 that

XX CC binds to MHC complex molecule, involving measuring the level of CTL

XX CC specific for CYP1B1 or the peptide of CYP1B1 in a sample from the patient

XX CC ; (2) a CYP1B1 peptide (I) that binds to MHC complex molecule; (3) an ex

XX CC vivo generated CTL (II) that specifically kills a cell expressing CYP1B1

XX CC in a specific of a MHC complex-restricted fashion; and (4) an ex vivo

XX CC generated APC (III) that presents a peptide of a CYP1B1 in the context of

XX CC a MHC complex molecule. The method is useful for treating a patient

XX CC having or is at risk of having a cell that expresses CYP1B1. The method

XX CC is useful for the prevention, treatment and diagnosis of cancer, e.g.

XX CC melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and

XX CC lung, ovarian, uterine, cervical, prostate, liver, colon, pancreatic and

XX CC brain cancer. AAM06905 to AAM13566 represent CYP1B1 peptides which can

XX CC bind to human leukocyte antigens (HLAs), as well as other amino acid

XX CC sequence used in the exemplification of the present invention

XX SQ Sequence 10 AA;

Query Match 41.5%; Score 34; DB 4; Length 10;

Best Local Similarity 60.0%; Pred. No. 72;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SFVSPRPLPV 14

:|: |||||

Db 1 AFLDPRPLTV 10

RESULT 14

AA013226

ID AAM13226 standard; peptide; 10 AA.

XX AC AAM13226;

XX DT 09-OCT-2001 (first entry)

XX DE HLA-A26 decamer #289.

XX KW Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA;

XX KW human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; APC;

XX KW major histocompatibility complex; antigen presenting cell; melanoma;

XX KW lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.

XX OS Homo sapiens.

XX PN WO200135810-A2.

XX PD 25-MAY-2001.

XX PF 15-NOV-2000; 2000WO-US031513.

XX PR 15-NOV-1999; 99US-0165590P.

XX PA (DAND) DANA FARBER CANCER INST INC.

XX PA (UYBO-) UNIV BOSTON.

XX PI Schultze JL, Vonderheide RH, Sherr D, Nadler LM, Maecker B;

XX PI Von Bergwelt- Balldon M;

XX DR WPI; 2001-355537/37.

XX PT Treating a cancer patient involves administering to patient a cytotoxic T

XX PT -lymphocyte, an antigen presenting cell that activates T cells, a peptide

XX PT of cytochrome P450 1B1, or a polynucleotide encoding the peptide.

XX PS Disclosure; Page 93; 121pp; English.

XX CC The present invention describes a method for treating a patient having,

XX CC or is at risk of having, a cell expressing cytochrome P450 1B1 (CYP1B1),

XX CC which involves administering to the patient a cytotoxic T-lymphocyte

XX CC (CTL) that kills the cell, an antigen presenting cell (APC) that

XX CC activates CTL, a peptide of CYP1B1 that binds to major histocompatibility

XX CC complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or

XX CC peptide of CYP1B1. Also described are: (1) a method for assessing the

XX CC level of immunity of a patient to CYP1B1 or a peptide of CYP1B1 that

XX CC binds to MHC complex molecule, involving measuring the level of CTL

XX CC specific for CYP1B1 or the peptide of CYP1B1 in a sample from the patient

XX CC ; (2) a CYP1B1 peptide (I) that binds to MHC complex molecule; (3) an ex

XX CC vivo generated CTL (II) that specifically kills a cell expressing CYP1B1

XX CC in a specific of a MHC complex-restricted fashion; and (4) an ex vivo

XX CC generated APC (III) that presents a peptide of a CYP1B1 in the context of

XX CC a MHC complex molecule. The method is useful for treating a patient

XX CC having or is at risk of having a cell that expresses CYP1B1. The method

XX CC is useful for the prevention, treatment and diagnosis of cancer, e.g.

XX CC melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and

XX CC lung, ovarian, uterine, cervical, prostate, liver, colon, pancreatic and

XX CC brain cancer. AAM06905 to AAM13566 represent CYP1B1 peptides which can

XX CC bind to human leukocyte antigens (HLAs), as well as other amino acid

XX CC sequence used in the exemplification of the present invention

XX SQ Sequence 10 AA;

Query Match 41.5%; Score 34; DB 4; Length 10;

Best Local Similarity 60.0%; Pred. No. 72;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SFVSPRPLPV 14

:|: |||||

Db 1 AFLDPRPLTV 10

Search completed: April 2, 2004, 10:08:42
Job time : 46 secs

Db 1 AFLDPRPLTV 10

RESULT 15
AAM11873
ID AAM11873 standard; peptide; 10 AA.
XX AC AAM11873;
XX AC AAM11873;
DT 09-OCT-2001 (first entry)
XX DE HLA-A *0202 decamer #110.
XX DE
XX KW Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis: HLA;
KW human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; APC;
KW major histocompatibility complex; antigen presenting cell; melanoma;
KW lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.
XX OS Homo sapiens.
XX OS
XX PN WO200135810-A2.
XX PD
XX PD 25-MAY-2001.
XX PF
XX PF 15-NOV-2000; 2000WO-US031513.
XX PR
XX PR 15-NOV-1999; 99US-0165590P.
XX PA (DAND) DANA FARMER CANCER INST INC.
XX PA (UYBO-) UNIV BOSTON.
XX PI
XX PI Schultze JL, Vonderheide RH, Sherr D, Nadler LM, Maecker B;
XX PI Von Bergwelt-Baildon M;
XX DR WPI; 2001-355537/37.
XX
XX Treating a cancer patient involves administering to patient a cytotoxic T
XX -lymphocyte, an antigen presenting cell that activates T cells, a peptide
XX of cytochrome P450 1B1, or a polynucleotide encoding the peptide.
XX
XX Disclosure; Page 84; 121pp; English.
XX
XX The present invention describes a method for treating a patient having,
XX or is at risk of having, a cell expressing cytochrome P450 1B1 (CYP1B1),
XX which involves administering to the patient a cytotoxic T-lymphocyte
XX (CTL) that kills the cell, an antigen presenting cell (APC) that
XX activates CTL, a peptide of CYP1B1 that binds to major histocompatibility
XX complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or
XX peptide of CYP1B1. Also described are: (1) a method for assessing the
XX level of immunity of a patient to CYP1B1 or a peptide of CYP1B1 that
XX binds to MHC complex molecule, involving measuring the level of CTL
XX specific for CYP1B1 or the peptide of CYP1B1 in a sample from the patient
XX ; (2) a CYP1B1 peptide (i) that binds to MHC complex molecule; (3) an ex
XX vivo generated CTL (ii) that specifically kills a cell expressing CYP1B1
XX in a specific of a MHC complex-restricted fashion; and (4) an ex vivo
XX generated APC (iii) that presents a peptide of a CYP1B1 in the context of
XX a MHC complex molecule. The method is useful for treating a patient
XX having or is at risk of having a cell that expresses CYP1B1. The method
XX is useful for the prevention, treatment and diagnosis of cancer, e.g.
XX melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and
XX lung, ovarian, uterine, cervical, prostate, liver, colon, pancreatic and
XX brain cancer. AAM06905 to AAM13566 represent CYP1B1 peptides which can
XX bind to human leukocyte antigens (HLAs), as well as other amino acid
XX sequence used in the exemplification of the present invention
XX
XX Sequence 10 AA;

Query Match 41.5%; Score 34; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 5 SFVSPRPLPV 14
: : | | | | |

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OM protein - protein search, using sw model

Run on: April 2, 2004, 09:58:38 ; Search time 7.66667 Seconds
(without alignments)
101.876 Million cell updates/sec

Title: US-10-009-049-1

Perfect score: 84

Sequence: 1 CRAHSFGSPRLPVV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 801

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	31.0	13	1 BP1 BOTJA	P01020 bothrops ja
2	26	31.0	15	1 UC29 MAIZE	P00635 zea mays (m
3	25	29.8	13	1 PSBP PINPS	P81668 pinus pinas
4	24	28.6	11	1 BPP3 BOTIN	P30423 bothrops in
5	24	28.6	11	1 BPP4 BOTIN	P30424 bothrops in
6	24	28.6	15	1 MK1 PALPR	P80408 palomona pr
7	24	28.6	15	1 MK2A PALPR	P80409 palomona pr
8	23	27.4	9	1 FAR9 ASCSU	P43172 ascaris suu
9	23	27.4	12	1 PSP3 PHYPA	P80662 physcomitre
10	22	26.2	8	1 ALL3 CYDPO	P82154 cydia pomon
11	22	26.2	8	1 ALL4 CALVO	P41840 calliphora
12	22	26.2	8	1 ALL4 CYDPO	P82155 cydia pomon
13	22	26.2	10	1 FAR6 PANFE	P82660 panagrellus
14	21	25.0	10	1 GLEM HUMAN	P02728 homo sapien
15	21	25.0	11	1 TIN4 HOPTI	P82654 hoplobatr
16	21	25.0	12	1 PK4 PERU	P82690 periplaneta
17	21	25.0	12	1 TIN2 HOPTI	P82652 hoplobatr
18	21	25.0	12	1 TIN3 HOPTI	P82653 hoplobatr
19	21	25.0	13	1 LMT4 LOGMI	P41490 locusta mig
20	21	25.0	14	1 EDCB LYMDI	P80940 lymantria d
21	21	25.0	15	1 PDGB PIG	P20034 sus scrofa
22	20	23.8	9	1 MGMT BOVIN	P29177 bos taurus
23	20	23.8	12	1 PK4 PERAM	P82619 periplaneta
24	20	23.8	15	1 METK MAIZE	P80616 zea mays (m
25	19	22.6	7	1 ALL2 CARMA	P81805 carcinus ma
26	19	22.6	8	1 ALL5 CYDPO	P82156 cydia pomon
27	19	22.6	8	1 LCK4 LEUMA	P21143 leucophaea
28	19	22.6	8	1 LCK6 LEUMA	P19988 leucophaea
29	19	22.6	9	1 XVL4 STRSQ	P19149 streptomyce
30	19	22.6	10	1 BPP2 BOTJA	P01022 bothrops ja
31	19	22.6	11	1 BPPB AGKHA	P01021 agkistrodon
32	19	22.6	11	1 TKNA CHICK	P19850 gallus gall
33	19	22.6	11	1 TKNA_GADMO	P28498 gadus morhu

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34 19 22.6 11 1 TKNA_ONCMY P28499 oncorhynchu
35 19 22.6 11 1 TKNA_SCYCA P41333 scyllorhinu
36 19 22.6 14 1 UC15_MAIZE P00621 zea mays (m
37 18 21.4 5 1 AL14_CARMA P81817 carcinus ma
38 18 21.4 8 1 AL15_CARMA P81818 carcinus ma
39 18 21.4 8 1 AL17_CARMA P81820 carcinus ma
40 18 21.4 8 1 AL18_CARMA P81821 carcinus ma
41 18 21.4 8 1 VGLG_HSV2B P81780 herpes simp
42 18 21.4 10 1 AL19_CARMA P81822 carcinus ma
43 18 21.4 10 1 FARP_MANSE P18523 manduca sex
44 18 21.4 10 1 PNEU_RAT P21996 rattus norv
45 18 21.4 13 1 TEMD_RANTE P56919 rana tempor

```

ALIGNMENTS

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RESULT 1
BP1 BOTJA STANDARD; PRT; 13 AA.
AC P01020; P30421;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S3,1 (13A) (Angiotensin-converting
DE enzyme inhibitor V-9).
OS Bothrops jararaca (Jararaca), and
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724, 8723;
RN [1]
RP SEQUENCE.
RC SPECIES=B.jararaca; TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=B.insularis; TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01253; XAVI9B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1388 MW; 6824FC97D83D6774 CRC64;
Query Match 31.0%; Score 26; DB 1; Length 13;
Best Local Similarity 55.6%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 7 GSPRLPVV 15
DB 3 GWPRGPEI 11
RESULT 2
UC29 MAIZE STANDARD; PRT; 15 AA.
ID UC29 MAIZE
AC P80635;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

```

DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 45)
DE (Fragment).
DE Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Fernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.9, its MW is: 37.6 kDa.
DR Maize-2DPAGE; P80635; COLEOPTILE.
FT NON_TER 1 15
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1679 MW; 3D53086B16019BC1 CRC64;
Query Match 31.0%; Score 26; DB 1; Length 15;
Best Local Similarity 42.9%; Pred. No. 2.7e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 8 SPRPLV 14
DB 1 NPNVPVI 7
RESULT 3
ID PSBP_PINPS STANDARD; PRT; 13 AA.
AC P81668;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Oxygen-evolving enhancer protein 2 (OEE2) (23 kDa subunit of oxygen
DE evolving system of photosystem II) (Fragment).
GN PSBP.
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- FUNCTION: May be involved in the regulation of photosystem II.
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
CC with the photosystem II complex (By similarity).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
CC (spot N179) is: 5.9, its MW is: 22 kDa.
CC -!- SIMILARITY: Belongs to the psbp family.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1294 MW; C6772B0D54D7C44D CRC64;
Query Match 29.8%; Score 25; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 AHSGSPR 10
DB 6 ANVFGAPK 13

RESULT 4
ID BPP3_BOTIN STANDARD; PRT; 11 AA.
AC P30423;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; C37196; C37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT MOD_RES 1 1
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;
Query Match 28.6%; Score 24; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 GSPRP 11
DB 3 GPPRP 7
RESULT 5
ID BPP4_BOTIN STANDARD; PRT; 11 AA.
AC P30424;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; D37196; D37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT MOD_RES 1 1
SQ SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

Query Match 28.6%; Score 24; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GSPRP 11
 ||||
 Db 3 GPRRP 7

RESULT 6

MK1_PALPR ID MK1_PALPR STANDARD; PRT; 15 AA.
 AC P80408;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Metainikowin I.
 OS Palomena prasina (Green shield bug).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
 OC Panheteroptera; Pentatomomorpha; Pentatomioidea; Pentatomidae;
 OC Palomena.
 OX NCBI_TaxID=55431;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RA Chernyeh S., Coccianich S., Briand J.-P., Hetru C., Bulet P.;
 RT "The inducible antibacterial peptides of the hemipteran insect
 Palomena prasina: identification of a unique family of proline-rich
 RT peptides and of a novel insect defensin.";
 RL J. Insect Physiol. 42:81-89(1996).
 CC -!- FUNCTION: Antibacterial peptide active against Gram-negative
 CC bacteria.
 CC -!- INDUCTION: By bacterial infection.
 KW Antibiotic; Insect immunity.
 SQ SEQUENCE 15 AA; 1838 MW; 21407E663CE46299 CRC64;

Query Match 28.6%; Score 24; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 PRPLP 13
 ||||
 Db 8 PRPRP 12

RESULT 7

MK2A_PALPR ID MK2A_PALPR STANDARD; PRT; 15 AA.
 AC P80409;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Metainikowin IIA.
 OS Palomena prasina (Green shield bug).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
 OC Panheteroptera; Pentatomomorpha; Pentatomioidea; Pentatomidae;
 OC Palomena.
 OX NCBI_TaxID=55431;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RA Chernyeh S., Coccianich S., Briand J.-P., Hetru C., Bulet P.;
 RT "The inducible antibacterial peptides of the hemipteran insect
 Palomena prasina: identification of a unique family of proline-rich
 RT peptides and of a novel insect defensin.";
 RL J. Insect Physiol. 42:81-89(1996).
 CC -!- FUNCTION: Antibacterial peptide active against Gram-negative
 CC bacteria.
 CC -!- INDUCTION: By bacterial infection.
 KW Antibiotic; Insect immunity.
 SQ SEQUENCE 15 AA; 1893 MW; 23835D063B946299 CRC64;

Query Match 28.6%; Score 24; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 PRPLP 13
 ||||
 Db 8 PRPWP 12

RESULT 8

FAR9_ASCSU ID FAR9_ASCSU STANDARD; PRT; 9 AA.
 AC P43172;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRamide-like neuropeptide AF9.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95380362; PubMed=7651904;
 RA Cowden C., Stretton A.O.W.;
 RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
 RT Ascaris suum.";
 RL Peptides 16:491-500(1995).
 CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 CC family.
 CC Neuropeptide; Amidation.
 KW MOD_RES 9
 FT SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 27.4%; Score 23; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPL 12
 ||||
 Db 4 PRPL 7

RESULT 9

PSP3_PHYPA ID PSP3_PHYPA STANDARD; PRT; 12 AA.
 AC P80562;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Oxygen-evolving enhancer protein 2 (OE2) (24 kDa subunit of oxygen
 DE evolving system of photosystem II) (Fragment).
 OS Physcomitrella patens (Moss).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 OX NCBI_TaxID=3218;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Protonema;
 RX MEDLINE=97275459; PubMed=9129336;
 RA Karsten B., Buck F., Nuske J., Reski R.;
 RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
 RT plastid enzymes.";
 RL Planta 201:261-272(1997).
 CC -!- FUNCTION: May be involved in the regulation of photosystem II.
 CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
 CC with the photosystem II complex.
 CC -!- INDUCTION: By light.
 CC -!- SIMILARITY: Belongs to the psbp family.
 CC Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane;
 KW Multigene family.
 FT NON_TER 12


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SQ SEQUENCE 12 AA; 1182 MW; 8D2B0D54D7C44DC5 CRC64;
Query Match 27.4%; Score 23; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 6.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AHSFGSP 9
Db 6 ANVFGAP 12

RESULT 10
ALL3_CVDPO
ID ALL3_CVDPO STANDARD; PRT; 8 AA.
AC P82154;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Cydiastatin 3.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=93282829;
RA Dave H., Johnsen A.H., Maestri J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
XW MOD RES 8
SQ SEQUENCE 8 AA; 926 MW; C82879D5AB477415 CRC64;

Query Match 26.2%; Score 22; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RAHSFG 7
Db 2 RPYSGF 7

RESULT 11
ALL4_CALVO
ID ALL4_CALVO STANDARD; PRT; 8 AA.
AC P41840;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Callatostatin 4 (Leu-callatostatin 4).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=93211980; PubMed=8460157;
RA Dave H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=94291167; PubMed=8020069;
RA Dave H., Thorpe A.;
RT "Distribution and functional significance of Leu-callatostatins in

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RT the blowfly Calliphora vomitoria.";
RL Cell Tissue Res. 276:367-379(1994).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator and play
CC a role in the integration of information within the brain. May be
CC involved in the control of visceral muscles due to its ability to
CC behave as potent inhibitors of peristaltic movements. May also
CC fulfill a neurohormonal role on muscles of the gut and heart.
CC -!- TISSUE SPECIFICITY: Brain, subesophageal ganglion, retrocerebral
CC complex, thoracic-abdominal ganglion, peripheral neurosecretory
CC system and intestine.
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
XW MOD RES 8
FT UNSURE 1
SQ SEQUENCE 8 AA; 954 MW; D32879D5AB47740A CRC64;

Query Match 26.2%; Score 22; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RAHSFG 7
Db 2 RPYSGF 7

RESULT 12
ALL4_CVDPO
ID ALL4_CVDPO STANDARD; PRT; 8 AA.
AC P82155;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 4.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=93282829;
RA Dave H., Johnsen A.H., Maestri J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
XW MOD RES 8
SQ SEQUENCE 8 AA; 910 MW; 922879D5AB47740D CRC64;

Query Match 26.2%; Score 22; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RAHSFG 7
Db 2 RPYSGF 7

RESULT 13
FAR6_PANRE
ID FAR6_PANRE STANDARD; PRT; 10 AA.
AC P82660;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRamide-like neuropeptide PFG (NGAPQPFVRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;

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RN  [1]
RP  SEQUENCE, FUNCTION, AND AMIDATION.
RA  Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RX  Maule A.G.;
RT  "Isolation, characterization and pharmacology of RMRFamide-related
RL  peptides (FaPe) from free-living nematode, Panagrellus redivivus.";
RT  Submitted (JUL-2000) to Swiss-Prot.
CC  -!- FUNCTION: Myoactive.
CC  -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC  family.
KW  Neuropeptide; Amidation.
FT  MOD RES 10 10 AMIDATION.
SQ  SEQUENCE 10 AA; 1132 MW; CB13B4C9D776C76D CRC64;

Query Match 26.2%; Score 22; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 7.6e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  7 GSPRP 11
DB  2 GAQOP 6

RESULT 14
GLEM_HUMAN
ID  GLEM_HUMAN STANDARD; PRT; 10 AA.
AC  P02728;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Erythrocyte membrane glycopeptide.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=72034940; PubMed=5286858;
RA  Weiss J.B., Lote C.J., Bobinski H.;
RT  "New low molecular weight glycopeptide containing triglycosylcysteine
RT  in human erythrocyte membrane.";
RL  Nature New Biol. 234:25-26(1971).
CC  -!- PTM: S-linked glycan consists of Glc-Glc-Glc trisaccharide.
CC  -!- MISCELLANEOUS: The identity of the glycoprotein from which this
CC  peptide is derived is unknown. No physiological function has been
CC  attributed.
DR  PIR; A03187; XGHUE.
KW  Glycoprotein; Erythrocyte.
FT  CARBOHYD 1 1 S-LINKED (GLC. . .).
SQ  SEQUENCE 10 AA; 1049 MW; 239BFEEA1F5B1E8 CRC64;

Query Match 25.0%; Score 21; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1 CRAHS 5
DB  1 CEGHS 5

RESULT 15
TINA_HOFTI
ID  TINA_HOFTI STANDARD; PRT; 11 AA.
AC  P82654;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Tigerin-4.
OS  Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
OC  Hoplobatrachus.
OX  NCBI_TaxID=103373;

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RN  [1]
RP  SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RX  TISSUE=Skin secretion;
RA  PubMed=11031261;
RA  Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA  Devi A.S., Nagaraj R., Sitaram N.;
RT  "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT  tigrina.";
RL  J. Biol. Chem. 276:2701-2707(2001).
CC  -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
CC  S.aureus, M.luteus, P.putida and S.cerevisiae.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Skin.
CC  -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
KW  Amphibian defense peptide; Antibiotic.
FT  DISULFID 3 11
SQ  SEQUENCE 11 AA; 1248 MW; 117D8EPD37605DCB CRC64;

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Query Match 25.0%; Score 21; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY  11 PLPV 14
DB  7 PLPI 10

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Search completed: April 2, 2004, 10:09:17
Job time : 8.66667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 09:56:18 ; Search time 46 Seconds
(without alignments)
92.135 Million cell updates/sec

Title: US-10-009-049-1

Perfect score: 84

Sequence: 1 CRAHFGSPRLPVV 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 447529

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	15	4	AAB59249 Peptide r
2	75	89.3	15	4	AAB59250 Peptide #
3	75	89.3	15	4	AAB59251 Peptide #
4	38	45.2	15	6	ABR44350 N-termina
5	37	44.0	15	5	AAB05069 Proline-r
6	36	42.9	15	5	ABG72660 Human K-r
7	35	41.7	13	2	AAW11111 Src SH3 d
8	34	40.5	9	2	AAW94619 Src homol
9	34	40.5	15	2	AAW39011 Peptide r
10	33	39.3	11	3	ABG06977 Epitope #
11	33	39.3	12	4	ABM00138 Amylase n
12	33	39.3	12	4	ABM00140 Amylase n
13	33	39.3	13	2	AAW11105 Src SH3 d
14	33	39.3	14	2	AAW11098 Src SH3 d
15	33	39.3	14	2	AAW25512 SH3 synth
16	33	39.3	14	4	AAW53295 Human non
17	32.5	38.7	15	2	AAW38981 Peptide r
18	32	38.1	10	4	AAW06985 CYP1B1 HL
19	32	38.1	10	4	AAW08985 HLA-A *02
20	32	38.1	10	4	AAW12950 HLA-A26 d
21	32	38.1	10	4	AAW08833 HLA-A1 de
22	32	38.1	10	4	AAW09489 HLA-B *07
23	32	38.1	11	5	AAU75613 Human non
24	32	38.1	12	3	AAW21272 ADAM 10/K
25	32	38.1	14	1	AAW60604 Sequence

ALIGNMENTS

RESULT 1
AAB59249
ID AAB59249 standard; peptide; 15 AA.

XX AC AAB59249;

XX DT 27-MAR-2001 (first entry)

XX DE Peptide recognised by gene VIII library clone 45.

XX KW Fibrin fragment E; cell proliferation; cancer; vascular restenosis;
XX arthritiis; diabetes; renal disease; psoriasis.

XX OS Synthetic.

XX PN WO200075175-A1.

XX PD 14-DEC-2000.

XX PF 07-JUN-2000; 2000WO-GB002197.

XX PR 07-JUN-1999; 99GB-00012994.

XX PA (UYAB-) UNIV ABERDEEN.

XX PI Melvin WT, Thompson WD, Stirk CM;

XX WPI; 2001-080581/09.

XX PT New peptides capable of modulating a fibrin fragment E activity, useful
XX for inhibiting uncontrolled cell proliferation, e.g. for treating cancer,
XX vascular restenosis, atherogenesis or psoriasis, and for wound healing.

XX Claim 1; Page 49; 59pp; English.

XX PS The present invention relates to a peptide or its fragment, which is
XX capable of modulating a fibrin fragment E activity. The peptides and
XX modulators are useful for inhibiting stimulation of cell proliferation
XX induced by a fibrin degradation product. The antibody or binding fragment
XX is also useful for identifying the active site of the fibrin fragment E
XX receptor. The peptides are particularly useful in treating cancer,
XX vascular restenosis, rheumatoid arthritis, diabetes, renal diseases or
XX psoriasis. The antibodies are also useful for modulating the activity of
XX the peptide

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 84; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRAHSGSPRLPVV 15
DB 1 CRAHSGSPRLPVV 15

RESULT 2
AAB59250
ID AAB59250 standard; peptide; 15 AA.
AC AAB59250;
XX
XX 27-MAR-2001 (first entry)
XX
XX Peptide #2 recognised by gene VIII library clone 45.
XX
XX Fibrin fragment E; cell proliferation; cancer; vascular restenosis;
KW arthritis; diabetes; renal disease; psoriasis.
XX
XX Synthetic.
XX
XX WO200075175-A1.
XX
XX 14-DEC-2000.
XX
XX 07-JUN-2000; 2000WO-GB002197.
XX
XX 07-JUN-1999; 99GB-00012994.
XX
XX (UYAB-) UNIV ABERDEEN.
XX
XX Melvin WT, Thompson WD, Stirk CM;
PI WPI; 2001-080581/09.
XX
XX New peptides capable of modulating a fibrin fragment E activity, useful
PT for inhibiting uncontrolled cell proliferation, e.g. for treating cancer,
PT vascular restenosis, atherogenesis or psoriasis, and for wound healing.
XX
XX Claim 1; Page 49; 59pp; English.
XX
XX The present invention relates to a peptide or its fragment, which is
CC capable of modulating a fibrin fragment E activity. The peptides and
CC modulators are useful for inhibiting stimulation of cell proliferation
CC induced by a fibrin degradation product. The antibody or binding fragment
CC is also useful for identifying the active site of the fibrin fragment E
CC receptor. The peptides are particularly useful in treating cancer,
CC vascular restenosis, rheumatoid arthritis, diabetes, renal diseases or
CC psoriasis. The antibodies are also useful for modulating the activity of
CC the peptide
XX
XX Sequence 15 AA;
SQ

Query Match 89.3%; Score 75; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAHSGSPRLPVV 15
DB 2 RAHSGSPRLPVV 15

RESULT 3
AAB59251
ID AAB59251 standard; peptide; 15 AA.
AC AAB59251;
XX
XX 27-MAR-2001 (first entry)
XX
XX Peptide #3 recognised by gene VIII library clone 45.
DE

XX Fibrin fragment E; cell proliferation; cancer; vascular restenosis;
KW arthritis; diabetes; renal disease; psoriasis.
XX
XX Synthetic.
XX
XX WO200075175-A1.
XX
XX 14-DEC-2000.
XX
XX 07-JUN-2000; 2000WO-GB002197.
XX
XX 07-JUN-1999; 99GB-00012994.
XX
XX (UYAB-) UNIV ABERDEEN.
XX
XX Melvin WT, Thompson WD, Stirk CM;
PI WPI; 2001-080581/09.
XX
XX New peptides capable of modulating a fibrin fragment E activity, useful
PT for inhibiting uncontrolled cell proliferation, e.g. for treating cancer,
PT vascular restenosis, atherogenesis or psoriasis, and for wound healing.
XX
XX Claim 1; Page 49; 59pp; English.
XX
XX The present invention relates to a peptide or its fragment, which is
CC capable of modulating a fibrin fragment E activity. The peptides and
CC modulators are useful for inhibiting stimulation of cell proliferation
CC induced by a fibrin degradation product. The antibody or binding fragment
CC is also useful for identifying the active site of the fibrin fragment E
CC receptor. The peptides are particularly useful in treating cancer,
CC vascular restenosis, rheumatoid arthritis, diabetes, renal diseases or
CC psoriasis. The antibodies are also useful for modulating the activity of
CC the peptide
XX
XX Sequence 15 AA;
SQ

Query Match 89.3%; Score 75; DB 4; Length 15;
Best Local Similarity 93.3%; Pred. No. 9.5e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRAHSGSPRLPVV 15
DB 1 CRAHSGSPRLPVV 15

RESULT 4
ABR44350
ID ABR44350 standard; peptide; 15 AA.
XX
XX ABR44350;
XX
XX 14-JUL-2003 (first entry)
XX
XX N-terminal sequence for guanosine triphosphate activator 10.01.
XX
XX Guanosine triphosphate activator 10.01; squamobasal cell;
KW carcinoma of skin; osteosarcoma; leukemia; teratoma.
XX
XX Unidentified.
XX
XX CN1380320-A.
XX
XX 20-NOV-2002.
XX
XX 10-APR-2001; 2001CN-00105912.
XX
XX 10-APR-2001; 2001CN-00105912.
XX
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX Mao Y, Xie Y;

XX WPI; 2003-222552/22.
XX A polypeptide-guanosine triphosphatase activator protein -10.01 and
PT polynucleotide for coding this polypeptide.
XX
XX Example 6; Page 21; 33pp; Chinese.
XX
XX The present invention discloses a polypeptide-guanosine triphosphatase
CC activator protein-10.01. The invention also discloses the method for
CC curing several diseases, such as squamous cell carcinoma of skin,
CC osteosarcoma, leukemia and teratoma by using said polypeptide. The
CC present sequence represents the N-terminal sequence of guanosine
CC triphosphate activator protein 10.01
XX
XX Sequence 15 AA;
SQ

Query Match 45.2%; Score 38; DB 6; Length 15;
Best Local Similarity 70.0%; Pred. No. 52;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 4 HSFQSPRLP 13
Db |||||:||||
4 HSLGLQLP 13

RESULT 5
AAW05069
ID AAW05069 standard; peptide; 15 AA.
XX
XX AAW05069;
XX
XX 25-MAR-2003 (revised)
DT 17-DEC-1996 (first entry)
XX
XX Proline-rich SH3 binding peptide fuse5B-4.51 from random library.
DE
XX
XX Src homology domain; SH3 domain; oncogene; consensus;
KW random display library.
KW
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH 7.13
FT /label= SH3 binding_motif
FT /note= "corresponds to consensus sequence RPLPXP"
FT
XX
XX US541109-A.
PN
XX
XX 30-JUL-1996.
PD
XX
XX 19-APR-1994; 94US-00230047.
PF
XX
XX 19-APR-1994; 94US-00230047.
PR
XX
XX (RHON) RHONE POULENC RORER PHARM INC.
PA
XX
XX Ivashchenko YD, Ricca GA, Cheadle C, South VJ, Jaye MC;
PI French SM, Searfoss GH;
PI
XX
XX WPI; 1996-361965/36.
DR
XX
XX New DNA encoding proteins that bind to Src-homology domain 3 - used to
PT inhibit signal transduction, e.g. in cases of T cell activation.
PT
XX
XX Example 1; Col 7; 39pp; English.
PS
XX

A fusion phase library for expressing random 15mer peptides was prepared
CC using the filamentous bacteriophage fuse 5B. The display library was
CC screened for peptides which bind to the Src SH3 domain. A sequence
CC comparison of the positive peptides revealed a highly reiterated, proline
CC -rich, 7 amino acid consensus motif (i.e. the sequence RPLPXP). This
CC motif demonstrated a strong similarity to a Src SH3 binding sequence

CC identified within a protein isolated by screening a lambda-lox mouse
CC embryo cDNA library with a Src SH3 domain probe. The present sequence is
CC that of one of the positive peptides identified from the fuse 5B random
CC display library. (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 15 AA;
SQ

Query Match 44.0%; Score 37; DB 2; Length 15;
Best Local Similarity 70.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 HSFQSPRLP 13
Db |||||:||||
1 HSHFHPRLP 10

RESULT 6
ABG72660
ID ABG72660 standard; peptide; 15 AA.
XX
XX ABG72660;
XX
XX 26-FEB-2003 (first entry)
DT
XX
XX Human K-ras 10.67 proto-oncogene protein, N-terminus.
DE
XX
XX Human; K-ras 10.67; proto-oncogene; tumour; haemopathy;
KW development disorder; human immunodeficiency virus infection; HIV;
KW immunological disease; inflammation.
KW
XX
XX Homo sapiens.
OS
XX
XX CN1352063-A.
PN
XX
XX 05-JUN-2002.
PD
XX
XX 02-NOV-2000; 2000CN-00127155.
PF
XX
XX 02-NOV-2000; 2000CN-00127155.
PR
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PA
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI; 2002-658691/71.
DR
XX
XX New human K-ras proto-oncogene protein 10.67 polypeptide for treating
PT malignant tumors, hemopathy, development disorder, human immunodeficiency
PT virus infection, immunological diseases and various inflammations.
PT
XX
XX Example 5; Page 19 (disclosure); 33pp; Chinese.
PS
XX
XX The present invention discloses a new kind of polypeptide, human K-ras
CC proto-oncogene protein 10.67, polynucleotides encoding the polypeptide
CC and a DNA recombination process to produce the polypeptide. The present
CC invention also discloses applying the polypeptide in treating various
CC diseases, such as malignant tumours, haemopathy, development disorder,
CC human immunodeficiency virus (HIV) infection, immunological diseases and
CC various inflammations. The present invention also discloses the
CC antagonist resisting the polypeptide and its treatment effect. The
CC present invention also discloses application of the polynucleotides
CC encoding human K-ras proto-oncogene protein 10.67. The present sequence
CC represents human K-ras proto-oncogene protein 10.67, N-terminus, used in
CC an ELISA (enzyme-linked immunosorbent assay) experiment
XX
XX Sequence 15 AA;
SQ

Query Match 42.9%; Score 36; DB 5; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 7 GSPRPLP 13
|||||

Db 8 GSPQPLP 14

RESULT 7
AAW11111
ID AAW11111 standard; peptide; 13 AA.
AC AAW11111;
XX
DT 25-JUN-1997 (first entry)
XX
DE Src SH3 domain-binding peptide used in signal transduction modulation.
XX
KW Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
KW protein tyrosine kinase; signal transduction; RNA processing;
KW trafficking; translation.
XX
OS Synthetic.
XX
PN WO9603649-A1.
XX
PD 08-FEB-1996.
XX
PF 24-JUL-1995; 95WO-US009382.
XX
PR 22-JUL-1994; 94US-00278865.
PR 07-JUN-1995; 95US-00483555.
XX
PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CJ;
XX
DR WPI; 1996-117151/12.
XX
PT Peptide with binding affinity for Src homology region 3 (SH3) domains of
PT proteins - useful for e.g. modulating signal transduction pathways at the
PT cellular level, esp. protein tyrosine kinase-mediated.
XX
PS Claim 38; Page 87; 116pp; English.
XX
CC AAW1098-W1124 are peptides that bind to the Src SH3 domain. The SH3
CC binding peptides are useful in modulating signal transduction pathways at
CC the cellular level (especially protein tyrosine kinase-mediated),
CC modulating oncogenic protein activity, or providing compounds for the
CC development of drugs with the ability to modulate broad classes, as well
CC as specific classes, of proteins involved in signal transduction and also
CC for regulating the processing, trafficking or translation of RNA.
CC Conjugates of the peptides with detectable labels or imaging agents are
CC useful for imaging cells, tissues and organs in which Src or Src-related
CC proteins are expressed
XX
SQ Sequence 13 AA;
Query Match 41.7%; Score 35; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLPW 15
Db :|||||:
2 TPRPLPI 9

RESULT 8
AAW94619
ID AAW94619 standard; peptide; 9 AA.
AC AAW94619;
XX
DT 29-APR-1999 (first entry)
XX
DE Src homology 3 domain binding nonamer peptide #1.
XX
KW Src homology 3 domain; SH3 domain; peptidomimetic; mimetic; modulator;

KW beta-turn template; spiro[pyrrolidine-2':3'-piperidin-2-ones];
KW fused ring analogue; signal transduction protein interaction;
KW inhibit cell growth; infection; cancer.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "acetylated"
XX
PN WO9854208-A1.
XX
PD 03-DEC-1998.
XX
PF 28-MAY-1998; 98WO-US010861.
XX
PR 28-MAY-1997; 97US-00864241.
PR 18-MAY-1998; 98US-0085989P.
XX
PA (CADU-) CADUS PHARM CORP.
XX
PI Castelhana AL, Witter DJ;
XX
DR WPI; 1999-080804/07.
XX
PT spiro[pyrrolidine-2':3'-piperidin-2-ones] and their fused ring analogues -
PT used, e.g. to modulate signal transduction protein interactions, inhibit
PT cell growth and for use in treating infections and cancer.
XX
PS Example 12; Page 59; 73pp; English.
XX
CC The present invention describes spiro[pyrrolidine-2':3'-piperidin-2-ones],
CC their fused ring analogues, and salts of both, all as individual
CC compounds or their libraries. They are peptidomimetics, and interact with
CC protein Src homology 3 (SH3) domains, involved in protein-protein
CC interactions in signal transduction. They cause disruption of the pathway
CC; in particular, they inhibit the protein tyrosine kinase system involved
CC in cell growth regulation. The cells may be microbial, e.g. pathogenic
CC bacterial or fungal cells responsible for infections, or of transformed
CC cells, e.g. responsible for neoplastic conditions. Specific examples of
CC Src proteins with SH3 domains are those known by the abbreviations p85,
CC Fyn, Lyn, Hck, Syk, Grb2, Gap, STAT, p47-phox, p67-phox, and Brk. The
CC present sequence represents a nonamer peptide used in an example from the
XX present invention
XX
SQ Sequence 9 AA;
Query Match 40.5%; Score 34; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
Db :|||||:
1 PRPLPV 6

RESULT 9
AAW39011
ID AAW39011 standard; peptide; 15 AA.
XX
AC AAW39011;
XX
DT 27-MAR-1998 (first entry)
XX
DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:410.
XX
KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl;
KW pLcGamma; p53bp2; Crk; Yes; Grb2.
XX
OS Synthetic.
XX
PN WO9730074-A1.

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XX PD 21-AUG-1997.
XX PF 14-FEB-1997; 97WO-US002298.
XX PR 16-FEB-1996; 96US-00602999.
XX PA (CYTO-) CYTOGEN CORP.
XX PA (UYNC-) UNIV NORTH CAROLINA.
XX PI Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CU, Fowlkes DM;
XX PI Rider JE;
XX DR WPI; 1997-424972/39.
XX CC The present sequence represents a peptide which resembles a Src homology
XX CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
XX CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
XX CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain
XX CC of Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which
XX CC bind the SH3 domain of p130Cas; (f) peptides which bind the SH3 domain
XX CC of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;
XX CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which
XX CC bind the amino-terminal SH3 domain of Grb2. The purified binding peptides
XX CC can be used in the method to identify inhibitors of their binding to
XX CC their respective SH3 domains, which could be used to modulate the
XX CC pharmacological activity of proteins or polypeptide containing the SH3
XX CC domain. The peptides can also be used to activate Src or Src-related
XX CC protein tyrosine kinases, to stimulate the immune response by increasing
XX CC the production of certain lymphokines, e.g. tumour necrosis factor-alpha
XX CC and interleukin-1, or to deliver a conjugated molecule to certain
XX CC cellular compartments containing Src or Src related proteins
XX SQ Sequence 15 AA;

Query Match 40.5%; Score 34; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
Db |||||
4 PRPLPV 9

RESULT 10
AAB06977
ID AAB06977 standard; peptide; 11 AA.
XX AC AAB06977;
XX DT 17-OCT-2000 (first entry)
XX DE Epitope # 7 from JE-1 (Natalase/ amylase).
XX KW Low allergenic protein variant; reduced immunogenicity;
XX KW allergy prevention; epitope; personal care product; enzyme;
XX KW food industry; textile industry; pharmaceutical; JE-1; natalase; amylase.
XX OS Unidentified.
XX PN WO200026230-A1.
XX PD 11-MAY-2000.
XX PF 12-OCT-1999; 99WO-DK000541.
XX PR 30-OCT-1998; 98DK-00001402.

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PR 25-NOV-1998; 98DK-00001645.
PR 04-OCT-1999; 99DK-00001417.
XX PA (NOVO ) NOVO NORDISK AS.
XX PI Roggen EL, Olsen AA, Ernst S;
XX DR WPI; 2000-365562/31.
XX PT Novel method for selecting low allergenic protein variants which are
XX PT useful in industrial, food, and pharmaceutical preparations.
XX PS Example 2; Page 66; 91pp; English.
XX CC The present invention relates to selecting a protein variant having
XX CC reduced immunogenicity as compared to a parent protein. The selected
XX CC proteins can be enzymes or peptide hormones. The proteins which are
XX CC selected are low allergenic proteins which can be used to prevent cases
XX CC of allergy in susceptible individuals. They can be used in the food or
XX CC textile industries, housekeeping, medicine, e.g. proteins used in
XX CC personal car products, and pharmaceuticals. The present sequence is an
XX CC epitope from JE-1 (Natalase/ amylase) parent protein. This sequence was
XX CC derived by screening a random peptide display library with
XX CC antibodies raised against JE-1. This sequence was then subjected to
XX CC genetical engineering mutations to reduce its immunogenicity. This
XX CC sequence was used in a sequence alignment to determine an epitope pattern
XX CC (AAB06998)
XX SQ Sequence 11 AA;

Query Match 39.3%; Score 33; DB 3; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRAHFGSPR 10
Db |||||
1 CNADSWGYP 10

RESULT 11
AAB00138
ID AAB00138 standard; peptide; 12 AA.
XX AC AAB00138;
XX DT 02-APR-2003 (first entry)
XX DE Amylase natalase antibody binding peptide sequence 24.
XX KW Allergen; protein coordinate data; vaccine; antiallergic; immunogenicity;
XX KW detergent; personal care composition; cosmetic.
XX OS Unidentified.
XX PN WO200183559-A2.
XX PD 08-NOV-2001.
XX PF 30-APR-2001; 2001WO-DK000293.
XX PR 28-APR-2000; 2000DK-00000707.
XX PR 10-MAY-2000; 2000US-0203345P.
XX PR 28-FEB-2001; 2001DK-00000327.
XX PR 21-MAR-2001; 2001US-0277817P.
XX PA (NOVO ) NOVOZYMES AS.
XX PI Roggen EL, Ernst S, Svendsen A, Friis EP, Von Der Osten C;
XX DR WPI; 2001-626552/72.
XX PT Selecting protein variants having modified immunogenicity, used to
XX PT produce vaccines, detergents and personal care compositions, involves

```

PT localizing epitope sequences on the three-dimensional structure of a
 XX protein.

PS Example 1; Page 148; 513pp; English.

XX The invention relates to selecting a protein variant having modified
 CC immunogenicity, compared to a parent protein, comprising using the
 CC antibody binding sequence to localise epitope sequences on the three
 CC dimensional structure of the parent protein and defining an epitope area
 CC including amino acids within 5 Angstrom of the epitope amino acids. The
 CC method is useful for identifying structural epitopes on the 3-dimensional
 CC surface of commercial and environmental allergens. Compositions
 CC containing the protein variants are used as vaccines, detergents and
 CC personal care compositions, e.g. shampoo, balsam, hair conditioners, hair
 CC waving compositions, hair dyeing compositions, hair tonic, hair liquid,
 CC hair cream, hair rinse, hair spray, chewing gum, skin cream, sunscreen,
 CC shaving foam, cream soap, skin milk or foundation. The present sequence
 CC is that of an antibody binding peptide sequence related to the invention

XX Sequence 12 AA;

Query Match 39.3%; Score 33; DB 4; Length 12;
 Best Local Similarity 60.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRAHSFGSPR 10
 | | | | |
 Db 1 CNADSWGYPYR 10

RESULT 12

ABM00140
 ID ABM00140 standard; peptide; 12 AA.

XX AC ABM00140;

DT 02-APR-2003 (first entry)

DE Amylase natalase antibody binding peptide sequence 26.

XX Allergen; protein coordinate data; vaccine; antiallergic; immunogenicity;
 KW detergent; personal care composition; cosmetic.

XX Unidentified.

XX WC200183559-A2.

XX 08-NOV-2001.

XX 30-APR-2001; 2001WO-DK000293.

XX 28-APR-2000; 2000DK-00000707.

XX 10-MAY-2000; 2000US-0203345P.

XX 28-FEB-2001; 2001DK-00000327.

XX 21-MAR-2001; 2001US-0277817P.

XX (NOVO) NOVOZYMES AS.

XX Roggen EL, Ernst S, Svendsen A, Friis EP, Von Der Osten C;

XX WPI; 2001-626552/72.

XX Selecting protein variants having modified immunogenicity, used to
 PT produce vaccines, detergents and personal care compositions, involves
 PT localizing epitope sequences on the three-dimensional structure of a
 PT protein.

XX Example 1; Page 148; 513pp; English.

XX The invention relates to selecting a protein variant having modified
 CC immunogenicity, compared to a parent protein, comprising using the
 CC antibody binding sequence to localise epitope sequences on the three
 CC dimensional structure of the parent protein and defining an epitope area

CC including amino acids within 5 Angstrom of the epitope amino acids. The
 CC method is useful for identifying structural epitopes on the 3-dimensional
 CC surface of commercial and environmental allergens. Compositions
 CC containing the protein variants are used as vaccines, detergents and
 CC personal care compositions, e.g. shampoo, balsam, hair conditioners, hair
 CC waving compositions, hair dyeing compositions, hair tonic, hair liquid,
 CC hair cream, hair rinse, hair spray, chewing gum, skin cream, sunscreen,
 CC shaving foam, cream soap, skin milk or foundation. The present sequence
 CC is that of an antibody binding peptide sequence related to the invention

XX Sequence 12 AA;

Query Match 39.3%; Score 33; DB 4; Length 12;
 Best Local Similarity 60.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRAHSFGSPR 10
 | | | | |
 Db 1 CNADSWGYPYR 10

RESULT 13

AAW11105

ID AAW11105 standard; peptide; 13 AA.

XX AC AAW11105;

DT 25-JUN-1997 (first entry)

DE Src SH3 domain-binding peptide used in signal transduction modulation.

XX Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
 KW protein tyrosine kinase; signal transduction; RNA processing;
 KW trafficking; translation.

XX Synthetic.

XX WO9603649-A1.

XX 08-FEB-1996.

XX 24-JUL-1995; 95WO-US009382.

XX 22-JUL-1994; 94US-00278865.

XX 07-JUN-1995; 95US-00483555.

XX (UYNC-) UNIV NORTH CAROLINA.

XX Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der Cü;

XX WPI; 1996-117151/12.

XX Peptide with binding affinity for Src homology region 3 (SH3) domains of
 PT proteins - useful for e.g. modulating signal transduction pathways at the
 PT cellular level, esp. protein tyrosine kinase-mediated.

XX Claim 38; Page 85; 116pp; English.

XX AAW11098-W11124 are peptides that bind to the Src SH3 domain. The SH3
 CC binding peptides are useful in modulating signal transduction pathways at
 CC the cellular level (especially protein tyrosine kinase-mediated),
 CC modulating oncogenic protein activity, or providing compounds for the
 CC development of drugs with the ability to modulate broad classes, as well
 CC as specific classes, of proteins involved in signal transduction and also
 CC for regulating the processing, trafficking or translation of RNA.
 CC Conjugates of the peptides with detectable labels or imaging agents are
 CC useful for imaging cells, tissues and organs in which Src or Src-related
 CC proteins are expressed

XX Sequence 13 AA;

Query Match 39.3%; Score 33; DB 2; Length 13;
 Best Local Similarity 62.5%; Pred. No. 2.7e+02;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLPV 15
 Db 2 TPRPLPML 9

RESULT 14
 AAW11098
 ID AAW11098 standard; peptide; 14 AA.
 XX
 AC AAW11098;
 XX
 DT 25-JUN-1997 (first entry)
 XX
 DE Src SH3 domain-binding peptide used in signal transduction modulation.
 XX
 KW Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
 KW protein tyrosine kinase; signal transduction; RNA processing;
 KW trafficking; translation.
 XX
 OS Synthetic.
 XX
 PN WO9603649-A1.
 XX
 PD 08-FEB-1996.
 XX
 PF 24-JUL-1995; 95WO-US009382.
 XX
 PR 22-JUL-1994; 94US-00278865.
 PR 07-JUN-1995; 95US-00483555.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX
 PI Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CJ;
 XX WPI; 1996-117151/12.
 DR
 PT Peptide with binding affinity for Src homology region 3 (SH3) domains of
 PT proteins - useful for e.g. modulating signal transduction pathways at the
 PT cellular level, esp. protein tyrosine kinase-mediated.
 XX
 PS Claim 32; Page 79; 116pp; English.
 XX
 CC AAW11098-W11124 are peptides that bind to the Src SH3 domain. The SH3
 CC binding peptides are useful in modulating signal transduction pathways at
 CC the cellular level (especially protein tyrosine kinase-mediated),
 CC modulating oncogenic protein activity, or providing compounds for the
 CC development of drugs with the ability to modulate broad classes, as well
 CC as specific classes, of proteins involved in signal transduction and also
 CC for regulating the processing, trafficking or translation of RNA.
 CC Conjugates of the peptides with detectable labels or imaging agents are
 CC useful for imaging cells, tissues and organs in which Src or Src-related
 CC proteins are expressed
 XX
 SQ Sequence 14 AA;
 Query Match 39.3%; Score 33; DB 2; Length 14;
 Best Local Similarity 62.5%; Pred. No. 2.9e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLPV 15
 Db 3 TPRPLPML 10

RESULT 15
 AAW25512
 ID AAW25512 standard; peptide; 14 AA.
 XX
 AC AAW25512;
 XX
 DT 27-MAR-1998 (first entry)

XX SH3 synthetic binding peptide.
 DE
 XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl;
 KW PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX
 OS Synthetic.
 XX
 PN WO9730074-A1.
 XX
 PD 21-AUG-1997.
 XX
 PF 14-FEB-1997; 97WO-US002298.
 XX
 PR 16-FEB-1996; 96US-00602999.
 XX
 PA (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX
 PI Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CJ, Fowlkes DM;
 PI Rider JE;
 XX
 DR WPI; 1997-424972/39.
 XX
 PT Src homology region 3 binding peptide - used to activate Src tyrosine
 PT kinase(s) and to stimulate immune response by increasing production of
 PT certain lymphokine(s), e.g. interleukin-1.
 XX
 PS Disclosure; Fig 7; 131pp; English.
 XX
 CC The present sequence represents a Src SH3 synthetic binding peptide. SH3
 CC (Src homology region 3) binding peptides are selected from: (a) peptides
 CC which bind the SH3 domain of Cortactin; (b) peptides which bind the
 CC middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl;
 CC (d) peptides which bind the SH3 domain of Src; (e) peptides which bind
 CC the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk; (h)
 CC peptides which bind the SH3 domain of Yes; and (i) peptides which bind
 CC the amino-terminal SH3 domain of Grb2. The purified binding peptides can
 CC be used in the method to identify inhibitors of their binding to their
 CC respective SH3 domains, which could be used to modulate the
 CC pharmacological activity of proteins or polypeptide containing the SH3
 CC domain. The peptides can also be used to activate Src or Src-related
 CC protein tyrosine kinases, to stimulate the immune response by increasing
 CC the production of certain lymphokines, e.g. tumour necrosis factor-alpha
 CC and interleukin-1, or to deliver a conjugated molecule to certain
 CC cellular compartments containing Src or Src related proteins
 XX
 .SQ Sequence 14 AA;
 Query Match 39.3%; Score 33; DB 2; Length 14;
 Best Local Similarity 62.5%; Pred. No. 2.9e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLPV 15
 Db 3 TPRPLPML 10

Search completed: April 2, 2004, 10:08:41
 Job time : 47 secs

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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:05:03 ; Search time 11 Seconds
(without alignments)
131.170 Million cell updates/sec

Title: US-10-009-049-1

Perfect score: 84

Sequence: 1 CKAHSGSPRLPVV 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2522

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	32.1	14	2 S27140	hypothetical prote
2	26	31.0	13	1 XAVI9B	angiotensin-conver
3	26	31.0	13	2 PA0089	protein QF200053 -
4	24	28.6	8	2 PH1618	Ig H chain V-D-J r
5	24	28.6	11	2 C37196	bradykinin-potenti
6	24	28.6	11	2 D37196	bradykinin-potenti
7	24	28.6	12	2 S43170	kinesin light chai
8	24	28.6	14	2 PA0013	photosystem II oxy
9	23	27.4	12	2 PH1457	T-cell receptor be
10	23	27.4	15	2 PA0060	protein QF200037 -
11	22.5	26.8	15	2 PS0452	32K protein 3306 -
12	22	26.2	7	2 S36662	dermorphin (Iys-7)
13	22	26.2	8	2 D47393	neuropeptide calla
14	22	26.2	13	2 FL0157	Ig kappa chain V-I
15	22	26.2	14	2 G44957	photosystem II oxy
16	21.5	25.6	13	2 IB4603	deoxynucleotidyltr
17	21	25.0	9	2 PT0238	Ig heavy chain CRD
18	21	25.0	10	2 XGHUE	erythrocyte membra
19	21	25.0	13	2 JH0460	corticostatic pept
20	21	25.0	13	2 B61620	locustamyotropin I
21	21	25.0	15	2 A22789	platelet-derived g
22	20	23.8	7	1 A61324	dermorphin - Rohde
23	20	23.8	9	4 S15594	orf 1 rara 5'-regi
24	20	23.8	10	2 PX0030	triacylglycerol li
25	20	23.8	11	2 I33098	17K exoantigen -
26	20	23.8	12	2 S01122	photosystem II 3.7
27	20	23.8	12	2 PH1459	T-cell receptor be
28	20	23.8	12	2 PH1468	T-cell receptor be
29	20	23.8	12	4 PC2121	aminotransferase c

30	20	23.8	15	2 S59492	formate dehydrogen
31	20	23.8	15	2 A40634	orf19 3' of eryk -
32	20	23.8	15	2 B32800	hypothetical prote
33	20	23.8	15	2 PX0031	mixed lymphocyte r
34	19	22.6	8	2 JS0316	leucokinin VI - Ma
35	19	22.6	9	2 A31576	xylose isomerase (
36	19	22.6	10	1 XAVI6B	angiotensin-conver
37	19	22.6	11	1 XASNBA	bradykinin-potenti
38	19	22.6	11	2 JN0023	substance P - chic
39	19	22.6	11	2 S23308	substance P - rain
40	19	22.6	11	2 S23306	substance R - Atla
41	19	22.6	11	2 S41476	probable antigen 5
42	19	22.6	11	2 S33300	probable substance
43	19	22.6	12	2 S26559	T-cell receptor be
44	19	22.6	12	2 S26554	T-cell receptor be
45	19	22.6	12	2 B49033	T-cell receptor de

ALIGNMENTS

RESULT 1

S27140
hypothetical protein 1 estrogen receptor 5'-region - human
C:Species: Homo sapiens (man)
C:Date: 05-Mar-1994 #sequence_revision 12-May-1995 #text_change 18-Aug-2000
C:Accession: S27140
R:Keaveney, M.; Klug, J.; Gannon, F.
DNA Seq. 2, 347-358, 1992
A:Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene
A:Reference number: S27140; MUID:93075998; PMID:1476547
A:Accession: S27140
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-14 <KEA>
A:Cross-references: EMBL:X62462; NID:G31201; PIDN:CAA44319.1; PID:G31202
C:Superfamily: unassigned leader peptides

Query Match 32.1%; Score 27; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAHSF 6

DB 2 RAHSF 6

RESULT 2

XAVI9B
angiotensin-converting enzyme inhibitor V-9 - jararaca
C:Species: Bothrops jararaca (Jararaca)
C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1991 #text_change 08-Dec-1995
C:Accession: A01253
R:Ondetti, M.A.; Williams, N.J.; Sabo, E.F.; Pluscec, J.; Weaver, E.R.; Kocy, O.
Biochemistry 10, 4033-4039, 1971
A:Title: Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. I
A:Reference number: A90356; MUID:72118526; PMID:4334402
A:Accession: A01253
A:Molecule type: protein
A:Residues: 1-13 <OND>
A:Note: the structure of the peptide was confirmed by synthesis
C:Comment: This peptide also potentiates bradykinin by inhibiting the kinases that inact
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

Query Match 31.0%; Score 26; DB 1; Length 13;

Best Local Similarity 55.6%; Pred. No. 4.8e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 GSPRPLPVV 15

DB 3 GWPAPGPEI 11

```

Db          3 GPPRP 7

RESULT 3
PA0089
Protein QF200053 - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0089
R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
Submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0051
A:Accession: PA0089
A:Molecule type: Protein
A:Residues: 1-13 <CHO>

Query Match      31.0%; Score 26; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          7 GSPPR 11
|:|||||
Db          5 GAPRP 9

RESULT 4
PH1618
Ig H chain V-D-J region (clone B-less 33) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1618
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1618
A:Molecule type: DNA
A:Residues: 1-8 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match      28.6%; Score 24; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY          1 CRAHSG 7
|:|||||
Db          1 CARHGYG 7

RESULT 5
C37196
bradykinin-potentiating peptide 3 - island jararaca
C:Species: Bothrops insularis (island jararaca)
C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C:Accession: C37196
R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides f
A:Reference number: A37196; MUID:90351557; PMID:2386615
A:Accession: C37196
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <CIN>
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match      28.6%; Score 24; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          7 GSPPR 11
|:|||||
Db          5 GAPRP 9

RESULT 6
D37196
bradykinin-potentiating peptide 4 - island jararaca
C:Species: Bothrops insularis (island jararaca)
C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C:Accession: D37196
R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides f
A:Reference number: A37196; MUID:90351557; PMID:2386615
A:Accession: D37196
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <CIN>
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match      28.6%; Score 24; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          7 GSPPR 11
|:|||||
Db          3 GPPRP 7

RESULT 7
S43170
kinesin light chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: S43170
R:Chernajovsky, Y.; Brown, A.; Jones, T.A.; Sheer, D.
Submitted to the EMBL Data Library, December 1992
A:Description: Promoter first exon/intron characterization and chromosomal location of t
A:Reference number: S43170
A:Accession: S43170
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <CHE>
A:Cross-references: EMBL:X69658; NID:g468786; PIDN:CAA49349.1; PID:g468787

Query Match      28.6%; Score 24; DB 2; Length 12;
Best Local Similarity 55.6%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY          2 RAHSFGSPR 10
|:|||||
Db          3 RGSSSGAPR 11

RESULT 8
PA0013
photosystem II oxygen-evolving complex protein 2 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C:Accession: PA0013
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
Submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional
A:Reference number: PA0001
A:Accession: PA0013
A:Molecule type: protein
A:Residues: 1-14 <KAM>
A:Experimental source: leaf
C:Keywords: photosynthesis; photosystem II

Query Match      28.6%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

QY 3 AHSFGSPR 10
| : | : | :
Db 6 ANVFGPK 13

RESULT 9

PH1457
T-cell receptor beta chain (clone A3/IC1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 17-Mar-1999
C:Accession: PH1457; S26542
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kojima, Y.; Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatibility complex peptides
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1457
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Experimental source: cytolytic T-lymphocyte, clone A3/IC1
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Widmer, J.; Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26542
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12 <CA2>
A:Cross-references: EMBL:X67992
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas2
C:Superfamily: immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 27.4%; Score 23; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AHSFGS 8
| : | : | :
Db 2 ASFGS 7

RESULT 10

PA0060
protein OF200037 - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0060
R:Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A:Reference number: PA0051
A:Accession: PA0060
A:Molecule type: protein
A:Residues: 1-15 <CHO>

Query Match 27.4%; Score 23; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 RPLP 13
| : | : | :
Db 3 RPLP 6

RESULT 11

PS0452
32K protein 3306 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C:Accession: PS0452
R:Tsugita, A.; Miyatake, N.
submitted to JIPID, April 1993

A:Reference number: PS0208
A:Accession: PS0452
A:Molecule type: protein
A:Residues: 1-15 <TSU>
A:Experimental source: bran, strain Nihonbare
C:Comment: molecular weight 32K, pI 5.3.

Query Match 26.8%; Score 22.5; DB 2; Length 15;
Best Local Similarity 45.5%; Pred. No. 2e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 5 SPGSPRPV 15
| : | : | :
Db 3 SPGSPRPV 10

RESULT 12

S36662
dermorphin (Iys-7) [validated] - two-colored leaf frog
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C>Date: 10-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 18-Aug-2000
C:Accession: S36662
R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.; FBBS Lett. 302, 151-154, 1992
A:Title: Identification and characterization of two dermorphins from skin extracts of the two-colored leaf frog
A:Reference number: S21152; MUID:92339502; PMID:1633846
A:Accession: S36662
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIG>
C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 26.2%; Score 22; DB 2; Length 7;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 HSFGSPR 10
| : | : | :
Db 1 YAFGPK 7

RESULT 13

D47393
neuropeptide callatostatin 4 - bluebottle fly (Calliphora vomitoria)
C:Species: Calliphora vomitoria
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995
C:Accession: D47393
R:Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobie, S.S.; Thorpe, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
A:Title: Callatostatin: neuropeptides from the blowfly Calliphora vomitoria with sequen
A:Reference number: A47393; MUID:93211980; PMID:8460157
A:Accession: D47393
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <DUV>
A:Experimental source: thoracic ganglia
A>Note: sequence extracted from NCBI backbone (NCBI:128479)

Query Match 26.2%; Score 22; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RAHSFG 7
| : | : | :
Db 2 RPYSGF 7

RESULT 14

PL0157
Ig kappa chain V-II region (antri-myelin-associated glycoprotein, PEC) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-Feb-1997
C:Accession: PL0157; C61458

R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
 J. Exp. Med. 170, 1551-1558, 1989
 A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-asso
 A:Reference number: A61458; MUID:90039128; PMID:2478651

A:Accession: PLO157
 A:Molecule type: protein
 A:Residues: 1-13 <BRO>
 A:Accession: C61458
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13 <BR2>
 C:Comment: This protein is one of monoclonal IgM reactive with myelin-associated glycop
 C:Keywords: glycoprotein; heterotetramer; immunoglobulin

Query Match 26.2%; Score 22; DB 2; Length 13;
 Best Local Similarity 71.4%; Pred. No. 2.1e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 SPRPLPV 14
 |||||
 Db 7 SPVTLPV 13

RESULT 15
 G44957
 Photosystem II oxygen-evolving complex protein 2 - common tobacco (cv. Samsun NN) (fragm
 C:Species: Nicotiana tabacum (common tobacco)
 C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Jun-1993
 C:Accession: G44957
 R:Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.
 Plant Cell Physiol. 31, 215-221, 1990
 A:Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabacum
 A:Reference number: A44957

A:Accession: G44957
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <TAK>

Query Match 26.2%; Score 22; DB 2; Length 14;
 Best Local Similarity 57.1%; Pred. No. 2.3e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AHSFGSP 9
 |||||
 Db 6 ANVFGKP 12

Search completed: April 2, 2004, 10:11:50
 Job time : 12 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:04:38 ; Search time 31.3333 Seconds
(without alignments)
151.046 Million cell updates/sec

Title: US-10-009-049-1
Perfect score: 84
Sequence: 1 CRAHSGSPRPLPV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3954

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_prodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	26	31.0	13 10 Q945C1	Q945C1 crypthecodi
2	26	31.0	14 11 Q8CJA8	Q8CJA8 mus musculu
3	26	31.0	15 11 Q8CJA9	Q8CJA9 mus musculu
4	25	29.8	14 8 Q98696	Q98696 hordium vul
5	25	29.8	15 8 Q95771	Q95771 ctenosaura
6	25	29.8	15 8 Q95952	Q95952 sauromalus
7	25	29.8	15 8 Q95879	Q95879 phrynosoma
8	25	29.8	15 8 Q95770	Q95770 cyclura ric
9	24	28.6	12 4 Q13865	Q13865 homo sapien
10	23	27.4	9 5 Q9TWV0	Q9TWV0 anthopleura
11	23	27.4	9 11 Q8CG39	Q8CG39 rattus norv
12	23	27.4	10 12 Q8JV78	Q8JV78 polyomaviru
13	23	27.4	13 11 Q88176	Q88176 mus musculu
14	22	26.2	8 10 Q8GTG5	Q8GTG5 lycopersico
15	22	26.2	11 2 Q9EUZ3	Q9EUZ3 escherichia
16	22	26.2	13 6 Q18890	Q18890 ateles belz

17	22	26.2	14 8 Q9G3C0	Q9G3C0 calliphora
18	21.5	25.6	13 4 Q14182	Q14182 homo sapien
19	21	25.0	10 10 Q9S905	Q9S905 glycine max
20	21	25.0	12 6 Q8MJE4	Q8MJE4 actus azara
21	21	25.0	13 7 Q9TNQ8	Q9TNQ8 homo sapien
22	21	25.0	13 11 Q9QV13	Q9QV13 cavia (guin
23	21	25.0	15 4 Q9UCC2	Q9UCC2 homo sapien
24	21	25.0	15 4 Q00604	Q00604 homo sapien
25	20	23.8	9 4 Q16220	Q16220 homo sapien
26	20	23.8	9 11 Q9QWTO	Q9QWTO mus musculu
27	20	23.8	11 2 Q7X566	Q7X566 thermus the
28	20	23.8	12 6 Q8MJQ0	Q8MJQ0 saquinus fu
29	20	23.8	12 6 Q8MJP8	Q8MJP8 callimico 9
30	20	23.8	12 6 Q8MJP7	Q8MJP7 callithrix
31	20	23.8	12 6 Q8MJP9	Q8MJP9 leontopithe
32	20	23.8	12 6 Q8MJE3	Q8MJE3 saimir sci
33	20	23.8	12 6 Q8MJQ1	Q8MJQ1 ateles fusc
34	20	23.8	12 6 Q8MJE2	Q8MJE2 cebus apell
35	20	23.8	12 11 Q9QVK4	Q9QVK4 rattus sp.
36	20	23.8	12 11 Q8R2F6	Q8R2F6 rattus norv
37	20	23.8	13 4 Q9UJ52	Q9UJ52 homo sapien
38	20	23.8	14 4 Q95179	Q95179 homo sapien
39	20	23.8	15 5 Q26323	Q26323 lymnaea sta
40	20	23.8	15 10 P82439	P82439 nicotiana t
41	20	23.8	15 11 Q9QZC9	Q9QZC9 mus musculu
42	19.5	23.2	13 5 Q818F3	Q818F3 drosophila
43	19	22.6	9 3 Q9F8E5	Q9F8E5 kluyveromyc
44	19	22.6	10 11 Q9QVF7	Q9QVF7 rattus sp.
45	19	22.6	12 4 Q9BZ49	Q9BZ49 homo sapien

ALIGNMENTS

RESULT 1
ID Q945C1 PRELIMINARY; PRT; 13 AA.
AC Q945C1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Dip5 protein (Fragment).
OS Cryptocodium cohnii (Dinoflagellate).
OC Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Cryptocodiaceae;
OC Cryptocodium.
OX NCBI_TaxID=2866;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21428164; PubMed=11545436;
RA Guillebault D., Derelle E., Bhaud Y., Moreau H.;
RT "Role of nuclear WW domains and proline-rich proteins in
RT dinoflagellate transcription.";
RL Protist 152:127-138(2001).
DR EMBL; AF417570; AAL15908.1; -.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1225 MW; 322FA05EE70CB327 CRC64;
Query Match 31.0%; Score 26; DB 10; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 5 SFGSPRPLP 13
Db 2 SSGPPKSLP 10
RESULT 2
ID Q8CJA8 PRELIMINARY; PRT; 14 AA.
AC Q8CJA8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Methylene tetrahydrofolate reductase short isoform (Fragment).
GN MTHFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=129/Sv;
RC MEDLINE=22257759; PubMed=12370778;
RX Tran P., Leclerc D., Chan M., Pai A., Hiou-Tim F., Wu Q., Goyette P.,
RA Artigas C., Milos R., Rozen R.;
RA "Multiple transcription start sites and alternative splicing in the
RT methylene tetrahydrofolate reductase gene result in two enzyme
RT isoforms.";
RL Mamm. Genome 13:483-492 (2002).
DR ENBL; AF404271; AAN40873.1; -;
DR MGD; MGI:106639; Mchfr.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1472 MW; 28DD341AC1695CB8 CRC64;
Query Match 31.0%; Score 26; DB 11; Length 14;
Best Local Similarity 55.6%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 AHSFGSPRP 11
DB 5 ARGSGSPNP 13
RESULT 3
Q8CJA9 PRELIMINARY; PRT; 15 AA.
ID Q8CJA9
AC Q8CJA9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Methylene tetrahydrofolate reductase short isoform (Fragment).
GN MTHFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=129/Sv;
RC MEDLINE=22257759; PubMed=12370778;
RX Tran P., Leclerc D., Chan M., Pai A., Hiou-Tim F., Wu Q., Goyette P.,
RA Artigas C., Milos R., Rozen R.;
RA "Multiple transcription start sites and alternative splicing in the
RT methylene tetrahydrofolate reductase gene result in two enzyme
RT isoforms.";
RL Mamm. Genome 13:483-492 (2002).
DR ENBL; AF404270; AAN40872.1; -;
DR MGD; MGI:106639; Mchfr.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1559 MW; 8D78DD341AC1695C CRC64;
Query Match 31.0%; Score 26; DB 11; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 AHSFGSPRP 11
DB 5 ARGSGSPNP 13
RESULT 4
O98696 PRELIMINARY; PRT; 14 AA.
ID O98696
AC O98696;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ORF321 protein (Fragment).
OS Hordeum vulgare (Barley).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Hassan; TISSUP=Leaf;
RA MEDLINE=20133023; PubMed=10666448;
RX del Campo E., Sabater B., Martin M.;
RA "Transcripts of the ndhH-D operon of barley plastids: possible role of
RT unedited site III in splicing of the ndhA intron.";
RL Nucleic Acids Res. 28:1092-1098 (2000).
DR ENBL; AJ011848; CAA09818.1; -;
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 1 1
SQ SEQUENCE 14 AA; 1521 MW; 361CF5911A68F8B8 CRC64;
Query Match 29.8%; Score 25; DB 8; Length 14;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 HSFSGS 8
DB 4 HSYGS 8
RESULT 5
Q95771 PRELIMINARY; PRT; 15 AA.
ID Q95771
AC Q95771;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 4 (Fragment).
GN ND4.
OS Ctenosaura similis (Spiny-tailed iguana).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Ctenosaura.
OX NCBI_TaxID=51212;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=97019047; PubMed=8865663;
RX Sites J.W. Jr., Davis S.K., Guerra T., Iverson J.B., Snell H.L.;
RA "Character congruence and phylogenetic signal in molecular and
RT morphological data sets: a case study in the living Iguanas (Squamata,
RT Iguanidae).";
RL Mol. Biol. Evol. 13:1087-1105 (1996).
DR ENBL; U66228; AAB07474.1; -;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1 1
SQ SEQUENCE 15 AA; 1853 MW; 8327178CA9352C01 CRC64;
Query Match 29.8%; Score 25; DB 8; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRAHS 5
DB 3 CRLHS 7
RESULT 6
Q95952 PRELIMINARY; PRT; 15 AA.
ID Q95952
AC Q95952;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)

DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE NADH dehydrogenase subunit 4 (Fragment).
 GN ND4.
 OS Sauromalus varius (San Esteban island chuckwalla).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Sauromalus.
 OX NCBI_TaxID=51220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97019047; PubMed=8865663;
 RA Sites J.W. Jr., Davis S.K., Guerra T., Iverson J.B., Snell H.L.;
 RT "Character congruence and phylogenetic signal in molecular and
 RT morphological data sets: a case study in the living Iguanas (Squamata,
 RT Iguanidae).";
 RL Mol. Biol. Evol. 13:1087-1105(1996).
 DR EMBL; U66223; AAB07480.1; -;
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1843 MW; 8327179CE9203901 CRC64;
 Query Match 29.8%; Score 25; DB 8; Length 15;
 Best Local Similarity 80.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRAHS 5
 Db |||||
 3 CRLHS 7
 RESULT 7
 Q95879 PRELIMINARY; PRT; 15 AA.
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE NADH dehydrogenase subunit 4 (Fragment).
 GN ND4.
 OS Phrynosoma cornutum (Texas horned lizard).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
 OC Phrynosoma
 OX NCBI_TaxID=43610;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97019047; PubMed=8865663;
 RA Sites J.W. Jr., Davis S.K., Guerra T., Iverson J.B., Snell H.L.;
 RT "Character congruence and phylogenetic signal in molecular and
 RT morphological data sets: a case study in the living Iguanas (Squamata,
 RT Iguanidae).";
 RL Mol. Biol. Evol. 13:1087-1105(1996).
 DR EMBL; U66224; AAB07478.1; -;
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1767 MW; 22C713C3138D16B7 CRC64;
 Query Match 29.8%; Score 25; DB 8; Length 15;
 Best Local Similarity 80.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRAHS 5
 Db |||||
 3 CRLHS 7
 RESULT 8
 Q95770 PRELIMINARY; PRT; 15 AA.
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DE NADH dehydrogenase subunit 4 (Fragment).
 GN ND4.
 OS Sauromalus varius (San Esteban island chuckwalla).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Sauromalus.
 OX NCBI_TaxID=51220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97019047; PubMed=8865663;
 RA Sites J.W. Jr., Davis S.K., Guerra T., Iverson J.B., Snell H.L.;
 RT "Character congruence and phylogenetic signal in molecular and
 RT morphological data sets: a case study in the living Iguanas (Squamata,
 RT Iguanidae).";
 RL Mol. Biol. Evol. 13:1087-1105(1996).
 DR EMBL; U66223; AAB07480.1; -;
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1843 MW; 8327179CE9203901 CRC64;
 Query Match 29.8%; Score 25; DB 8; Length 15;
 Best Local Similarity 80.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRAHS 5
 Db |||||
 3 CRLHS 7
 RESULT 9
 Q13865 PRELIMINARY; PRT; 12 AA.
 ID Q13865
 AC Q13865
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Kinesin light chain.
 GN BETA-KINESIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Placenta;
 RC MEDLINE=97101110; PubMed=8945637;
 RA Chernajovsky Y., Brown A., Jones T.A.;
 RT "Promoter first exon/intron characterization and chromosomal location
 RT of the human light chain (beta) kinesin gene.";
 RL DNA Cell Biol. 15:965-974(1996).
 DR EMBL; X69658; CAA49349.1; -;
 DR PIR; S43170; S43170.
 SQ SEQUENCE 12 AA; 1274 MW; 3FB8D34EE165A5B8 CRC64;
 Query Match 28.6%; Score 24; DB 4; Length 12;
 Best Local Similarity 55.6%; Pred. No. 2.5e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 RAHSFGSPR 10
 Db |||||
 3 RGSFGSPR 11
 RESULT 10
 Q9TWV0 PRELIMINARY; PRT; 9 AA.
 ID Q9TWV0
 AC Q9TWV0
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

AC Q95770;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE NADH dehydrogenase subunit 4 (Fragment).
 GN ND4.
 OS Cyclura ricordi (Ricord's rock iguana).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Cyclura.
 OX NCBI_TaxID=51215;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97019047; PubMed=8865663;
 RA Sites J.W. Jr., Davis S.K., Guerra T., Iverson J.B., Snell H.L.;
 RT "Character congruence and phylogenetic signal in molecular and
 RT morphological data sets: a case study in the living Iguanas (Squamata,
 RT Iguanidae).";
 RL Mol. Biol. Evol. 13:1087-1105(1996).
 DR EMBL; U66237; AAB07473.1; -;
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1715 MW; 8327178E7927A57E CRC64;
 Query Match 29.8%; Score 25; DB 8; Length 15;
 Best Local Similarity 80.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRAHS 5
 Db |||||
 3 CRLHS 7
 RESULT 9
 Q13865 PRELIMINARY; PRT; 12 AA.
 ID Q13865
 AC Q13865
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Kinesin light chain.
 GN BETA-KINESIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Placenta;
 RC MEDLINE=97101110; PubMed=8945637;
 RA Chernajovsky Y., Brown A., Jones T.A.;
 RT "Promoter first exon/intron characterization and chromosomal location
 RT of the human light chain (beta) kinesin gene.";
 RL DNA Cell Biol. 15:965-974(1996).
 DR EMBL; X69658; CAA49349.1; -;
 DR PIR; S43170; S43170.
 SQ SEQUENCE 12 AA; 1274 MW; 3FB8D34EE165A5B8 CRC64;
 Query Match 28.6%; Score 24; DB 4; Length 12;
 Best Local Similarity 55.6%; Pred. No. 2.5e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 RAHSFGSPR 10
 Db |||||
 3 RGSFGSPR 11
 RESULT 10
 Q9TWV0 PRELIMINARY; PRT; 9 AA.
 ID Q9TWV0
 AC Q9TWV0
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE Antho-RPAMIDE-NEUROPEPTIDE.
 OS Anthopleura elegansissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthae; Actiniidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=93126143; PubMed=1480510;
 RA Carlsensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;
 RT "Isolation of Leu-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH2 (Antho-RPamide),
 an N-terminally protected, biologically active neuropeptide from sea
 anemones.";
 RL Peptides 13; 851-857 (1992).
 SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;
 Query Match 27.4%; Score 23; DB 5; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 PRPLP 13
 Db 3 PGPLP 7
 RESULT 11
 Q8CG39 PRELIMINARY; PRT; 9 AA.
 ID Q8CG39
 AC Q8CG39
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Histamine N-tele-methyltransferase (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=96342418; PubMed=8750786;
 RA Takemura M., Yamauchi K., Yamatodani A.;
 RT "Structural analysis of histamine N-methyltransferase gene.";
 RL Methods Find. Exp. Clin. Pharmacol. 17:1-4(1995).
 DR EMBL; S82579; AAN86745.1; --
 DR GO; GO:0008168; F:methyltransferase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 KW Transferase; Methyltransferase.
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 1060 MW; 4223B1E042CEB053 CRC64;
 Query Match 27.4%; Score 23; DB 11; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CRAHSP 6
 Db 4 CVHSP 9
 RESULT 12
 Q8JUV78 PRELIMINARY; PRT; 10 AA.
 ID Q8JUV78
 AC Q8JUV78
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Large T antigen (fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=USA1;
 RX MEDLINE=21465052; PubMed=11581397;
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 RA Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 gastrointestinal tract after exposure to virions or viral DNA.";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL; AF303946; AAW97796.1; --
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1183 MW; 4CD6A96731A32763 CRC64;
 Query Match 27.4%; Score 23; DB 12; Length 10;
 Best Local Similarity 50.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 6 FGSPREL 13
 Db 1 FKPKTLP 8
 RESULT 13
 O88176 PRELIMINARY; PRT; 13 AA.
 ID O88176
 AC O88176
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Neural cell adhesion molecule (fragment).
 GN NCAM1 OR NCAM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Balb-C; TISSUE=Liver;
 RX MEDLINE=98250618; PubMed=9562442;
 RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
 RT "A cis-acting regulatory element that affects the alternative splicing
 of a muscle-specific exon in the mouse NCAM gene.";
 RL Biochim. Biophys. Acta 1397:305-315(1998).
 DR EMBL; AB001873; BAA31275.1; --
 DR MGD; MGI:97281; Ncam1.
 FT NON_TER 1
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;
 Query Match 27.4%; Score 23; DB 11; Length 13;
 Best Local Similarity 80.0%; Pred. No. 4e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 11 PLPVV 15
 Db 3 PLPVL 7
 RESULT 14
 Q8GTG5 PRELIMINARY; PRT; 8 AA.
 ID Q8GTG5
 AC Q8GTG5;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE WRKY transcription factor lrid-1 splice variant 2 (fragment).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Money Maker; TISSUE=Leaf;

RA Cagna G., Boes A., Ulker B., Zhou A., Wanke D., Somssich I.E.;
 RT "Comparison of WRKY group II transcription factors from plants."
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY157059; AAN71729.1; -.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 917 MW; 59177B475B87330 CRC64;

Query Match 26.2%; Score 22; DB 10; Length 8;
 Best Local Similarity 80.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GSPRP 11
 ||||
 Db 3 GSPYP 7

RESULT 15

Q9EUZ3 PRELIMINARY; PRT; 11 AA.
 AC Q9EUZ3;
 DT 01-MAR-2001 (TREMELrel. 16, Created)
 DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
 DE Ribosome binding factor A (Fragment).
 GN RBFA.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IQ490;
 RA Hedegaard J., Kristensen J.E., Nakamura Y., Sperling-Petersen H.U.,
 RA Mortensen K.K.;
 RT "Sequence of the infB gene from Escherichia coli strain IQ489 and
 RT IQ490."
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ132862; CAC20133.1; -.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1319 MW; 6B234CFE740879CB CRC64;

Query Match 26.2%; Score 22; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 5e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 AHSFGSPR 10
 ||||
 Db 2 AKEFGRPQ 9

Search completed: April 2, 2004, 10:11:05
 Job time : 33.3333 secs

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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:06:43 ; Search time 14 seconds
(without alignments)
55.314 Million cell updates/sec

Title: US-10-009-049-1

Perfect score: 84

Sequence: 1 CRAHSFGSPRLP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 146418

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep:*
 - 2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep:*
 - 3: /cgn2_6/ptodata/2/iaa/6A-COMB.pep:*
 - 4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep:*
 - 5: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.pep:*
 - 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	37	44.0	15	1	US-08-230-047-30
2	35	41.7	13	3	US-08-602-999A-92
3	35	41.7	13	4	US-08-278-865-92
4	35	41.7	13	4	US-09-500-124-92
5	34	40.5	9	4	US-09-086-1683-3
6	34	40.5	11	1	US-08-336-343A-29
7	34	40.5	11	3	US-08-652-877-29
8	34	40.5	11	3	US-08-476-515A-29
9	34	40.5	11	4	US-09-845-917A-17
10	34	40.5	12	3	US-08-602-999A-255
11	34	40.5	12	4	US-09-500-124-255
12	34	40.5	15	3	US-08-602-999A-410
13	34	40.5	15	4	US-09-500-124-410
14	33	39.3	11	4	US-09-417-608A-76
15	33	39.3	13	3	US-08-602-999A-86
16	33	39.3	13	4	US-08-278-865-86
17	33	39.3	13	4	US-09-500-124-86
18	33	39.3	14	3	US-08-602-999A-62
19	33	39.3	14	4	US-08-278-865-62
20	33	39.3	14	4	US-09-500-124-62
21	32.5	38.7	15	3	US-08-602-999A-378
22	32.5	38.7	15	4	US-09-500-124-378
23	31	36.9	11	4	US-07-756-641-18
24	31	36.9	12	1	US-07-756-250-3
25	31	36.9	14	3	US-08-602-999A-67
26	31	36.9	14	4	US-08-278-865-67
27	31	36.9	14	4	US-09-500-124-67

28	31	36.9	15	1	US-08-230-047-29	Sequence 29, Appl
29	31	36.9	15	3	US-09-045-632-103	Sequence 103, App
30	31	36.9	15	3	US-08-602-999A-355	Sequence 355, App
31	31	36.9	15	4	US-09-500-124-355	Sequence 355, App
32	30	35.7	11	1	US-08-336-343A-24	Sequence 24, Appl
33	30	35.7	11	3	US-08-652-877-34	Sequence 34, Appl
34	30	35.7	11	3	US-08-652-877-36	Sequence 36, Appl
35	30	35.7	11	3	US-08-476-515A-34	Sequence 36, Appl
36	30	35.7	11	3	US-08-602-999A-281	Sequence 281, App
37	30	35.7	12	3	US-08-602-999A-281	Sequence 281, App
38	30	35.7	12	4	US-09-500-124-281	Sequence 85, Appl
39	30	35.7	13	3	US-08-602-999A-85	Sequence 85, Appl
40	30	35.7	13	4	US-08-278-865-85	Sequence 85, Appl
41	30	35.7	13	4	US-09-500-124-85	Sequence 301, App
42	30	35.7	15	3	US-08-602-999A-301	Sequence 301, App
43	30	35.7	15	4	US-09-500-124-301	Sequence 83, Appl
44	29	34.5	9	2	US-08-765-783A-83	Sequence 83, Appl
45	29	34.5	9	3	US-09-416-557-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1
US-08-230-047-30
; Sequence 30, Application US/08230047
; Patent No. 5541109
; GENERAL INFORMATION:
; APPLICANT: Searfoss III, George H.
; APPLICANT: Ivashchenko, Yuri D.
; APPLICANT: Jave, Michael C.
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3043
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/230,047
; FILING DATE: 19-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: A1465-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-230-047-30

Query Match 44.0%; Score 37; DB 1; Length 15;
Best Local Similarity 70.0%; Pred No. 21;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 HSFSGSPRLP 13
|||
DB 1 HSHFPRPLP 10

RESULT 2
US-08-602-999A-92
; Sequence 92, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-92
Query Match 41.7%; Score 35; DB 3; Length 13;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 8 SPRPLPV 15
Db 2 TPRPLFI 9
RESULT 3
US-08-278-865-92
; Sequence 92, Application US/08278865
; Patent No. 6303574
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; APPLICANT: SPARKS, ANDREW B.
; APPLICANT: THORN, JUDITH M.
; APPLICANT: QUILLIAM, LAWRENCE A.
; APPLICANT: DER, CHANNING J.
; TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,865
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-007-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-278-865-92
Query Match 41.7%; Score 35; DB 4; Length 13;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 8 SPRPLPV 15
Db 2 TPRPLFI 9
RESULT 4
US-09-500-124-92
; Sequence 92, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-92

Query Match 41.7%; Score 35; DB 4; Length 13;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLPV 15
Db 2 TPRPLPI 9

RESULT 5
US-09-086-168B-3
; Sequence 3, Application US/09086168B
; Patent No. 6638941
; GENERAL INFORMATION:
; APPLICANT: Castelghano, Arindo
; APPLICANT: Witter, David
; TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED PEPTIDOMIMETICS AS BETA-TURN
; FILE REFERENCE: 60394-B
; CURRENT APPLICATION NUMBER: US/09/086,168B
; CURRENT FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SH3 test peptide
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Synthetic Peptide
US-09-086-168B-3

Query Match 40.5%; Score 34; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
Db 1 PRPLPV 6

RESULT 6
US-08-336-343A-29
; Sequence 29, Application US/08336343A
; Patent No. 5671144
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Alves, Frauke
; TITLE OF INVENTION: CCK-2, A No. 5677144e1 Receptor Tyrosine Kinase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York

```

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; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,343A
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-336-343A-29

Query Match 40.5%; Score 34; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
Db 2 PRPLPV 7

RESULT 7
US-08-652-877-29
; Sequence 29, Application US/08652877
; Patent No. 6187548
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjaln, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd., 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.5.1
; SOFTWARE: Word 6.0 (patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,877
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15203
; FILING DATE: 22-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836

```

/ FILING DATE: 23-NOV-1994
/ PRIOR APPLICATION DATA: US 08/487,314
/ APPLICATION NUMBER: 07-JUNE-1995
/ FILING DATE: 07-JUNE-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Savitzky, Martin
/ REGISTRATION NUMBER: 29,699
/ REFERENCE/DOCKET NUMBER: A1355E-US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-454-3816
/ TELEFAX: 610-454-3808
/ INFORMATION FOR SEQ ID NO: 29:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/ FRAGMENT TYPE: internal
/ US-08-652-877-29

Query Match 40.5%; Score 34; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
DB 2 PRPLPV 7

RESULT 8
US-08-476-515A-29
/ Sequence 29, Application US/08476515A
/ Patent No. 6239270
/ GENERAL INFORMATION:
/ APPLICANT: Akerstrom, Goran
/ APPLICANT: Juhlin, Claes
/ APPLICANT: Rask, Lars
/ APPLICANT: Crumley, Gregg R.
/ APPLICANT: Morse, Clarence C.
/ APPLICANT: Murray, Edward M.
/ APPLICANT: Hjalms, Goran
/ TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
/ TITLE OF INVENTION: Thereof and DNA Encoding Same
/ NUMBER OF SEQUENCES: 84
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Martin Savitzky
/ STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.,
/ STREET: 3C43,
/ CITY: Collegeville
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19426-0107
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Compaq PC
/ OPERATING SYSTEM: Windows 95
/ SOFTWARE: Word 7.0 (Patentin)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/476,515A
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/344,836
/ FILING DATE: 23-NOV-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/SE94/00483
/ FILING DATE: 24-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: SE 9301764-8
/ FILING DATE: 24-MAY-1993
/ ATTORNEY/AGENT INFORMATION:

/ NAME: Savitzky, Martin
/ REGISTRATION NUMBER: 29,699
/ REFERENCE/DOCKET NUMBER: A1355D
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-454-3816
/ TELEFAX: 610-454-3808
/ INFORMATION FOR SEQ ID NO: 29:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/ FRAGMENT TYPE: internal
/ US-08-476-515A-29

Query Match 40.5%; Score 34; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
DB 2 PRPLPV 7

RESULT 9
US-09-845-917A-17
/ Sequence 17, Application US/09845917A
/ Patent No. 6653529
/ GENERAL INFORMATION:
/ APPLICANT: Bogaert, Thierry
/ APPLICANT: Vandekerckhove, Joel
/ TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
/ TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
/ TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
/ FILE REFERENCE: P/14-1
/ CURRENT APPLICATION NUMBER: US/09/845,917A
/ CURRENT FILING DATE: 2001-04-30
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: Patent in Ver. 2.1
/ SEQ ID NO 17
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
/ US-09-845-917A-17

Query Match 40.5%; Score 34; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
DB 2 PRPLPV 7

RESULT 10
US-08-602-999A-255
/ Sequence 255, Application US/08602999A
/ Patent No. 6184205
/ GENERAL INFORMATION:
/ APPLICANT: SPARKS, Andrew B.
/ APPLICANT: KAY, Brian K.
/ APPLICANT: THORN, Judith M.
/ APPLICANT: QUILLIAM, Lawrence A.
/ APPLICANT: DER, Channing J.
/ APPLICANT: FOWLKES, Dana M.
/ APPLICANT: RIDER, James E.
/ TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
/ TITLE OF INVENTION: ISOLATING AND USING SAME
/ NUMBER OF SEQUENCES: 467
/ CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 16-FEB-1996
APPLICATION NUMBER: US/08/602,999A
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 255:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-255

Query Match 40.5%; Score 34; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
DB 3 PRPLPV 8

RESULT 11
US-09-500-124-255
Sequence 255, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 16-FEB-1996
APPLICATION NUMBER: US/09/500,124
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/602,999

FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 255:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-255

Query Match 40.5%; Score 34; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
DB 3 PRPLPV 8

RESULT 12
US-08-602-999A-410
Sequence 410, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 16-FEB-1996
APPLICATION NUMBER: US/08/602,999A
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 410:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-410

Query Match 40.5%; Score 34; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
| | | | |
Db 4 PRPLPV 9

RESULT 13

US-09-500-124-410
; Sequence 410, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELECOMUNICATION INFORMATION:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 410:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-410

Query Match 40.5%; Score 34; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
| | | | |
Db 4 PRPLPV 9

RESULT 14

US-09-417-608A-76
; Sequence 76, Application US/09417608A
; Patent No. 668164
; GENERAL INFORMATION:

; APPLICANT: Olsen, Arne
; APPLICANT: Roggen, Erwin
; APPLICANT: Ernst, Steffen
; TITLE OF INVENTION: Low Allergenic Protein Variants
; FILE REFERENCE: 5676.200-US
; CURRENT APPLICATION NUMBER: US/09/417,608A
; CURRENT FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patent in version 3.2
; SEQ ID NO: 76
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-417-608A-76

Query Match 39.3%; Score 33; DB 4; Length 11;
Best Local Similarity 60.0%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRAHSGSPR 10
| | | | |
Db 1 CNADSWGYP 10

RESULT 15

US-08-602-999A-86
; Sequence 86, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-86

Query Match 39.3%; Score 33; DB 3; Length 13;
 Best Local Similarity 62.5%; Pred. No. 71;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SPRPLPVV 15
 :|||||:
 Db 2 TPRPLPML 9

Search completed: April 2, 2004, 10:12:44
 Job time : 14 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 2, 2004, 10:11:14 ; Search time 32.333 Seconds
(without alignments)
121.720 Million cell updates/sec

Title: US-10-009-049-1

Perfect score: 84

Sequence: 1 CRAHSFGSPRLPVV 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1070241 seqs, 262374223 residues

Total number of hits satisfying chosen parameters: 173041

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	41.7	13	9	US-09-938-315-92
2	35	41.7	13	14	US-10-161-791-92
3	34	40.5	11	10	US-09-945-917-17
4	34	40.5	11	10	US-09-845-917A-17
5	34	40.5	12	14	US-10-161-791-255
6	34	40.5	15	14	US-10-161-791-410
7	33	39.3	13	9	US-09-938-315-86
8	33	39.3	13	14	US-10-161-791-86
9	33	39.3	14	9	US-09-938-315-62
10	33	39.3	14	14	US-10-161-791-62
11	32.5	38.7	15	14	US-10-161-791-378
12	32	38.1	15	14	US-10-059-261-8
13	32	38.1	15	14	US-10-059-261-116
14	31	36.9	14	9	US-09-938-315-67
15	31	36.9	14	14	US-10-161-791-67

16	31	36.9	15	14	US-10-161-791-355
17	30	35.7	8	9	US-09-815-837-114
18	30	35.7	11	15	US-10-149-138-4631
19	30	35.7	12	14	US-10-286-457-30
20	30	35.7	12	14	US-10-161-791-281
21	30	35.7	13	9	US-09-938-315-85
22	30	35.7	13	14	US-10-161-791-85
23	30	35.7	14	10	US-09-966-459A-37
24	30	35.7	14	12	US-10-308-128-60
25	30	35.7	15	14	US-10-001-469-2561
26	30	35.7	15	14	US-10-001-469-2642
27	30	35.7	15	14	US-10-161-791-301
28	29	34.5	9	9	US-09-730-857-83
29	29	34.5	9	12	US-10-601-837-101
30	29	34.5	10	10	US-09-572-404B-1382
31	29	34.5	10	10	US-09-572-404B-1384
32	29	34.5	10	10	US-09-572-404B-1593
33	29	34.5	10	14	US-10-044-896-9
34	29	34.5	12	10	US-09-291-417-78
35	29	34.5	12	10	US-09-291-417-114
36	29	34.5	12	14	US-10-158-596A-14
37	29	34.5	12	14	US-10-157-775B-14
38	29	34.5	12	14	US-10-254-446A-14
39	29	34.5	12	14	US-10-155-883B-14
40	29	34.5	13	14	US-10-193-477-59
41	29	34.5	14	14	US-10-185-050-223
42	28.5	33.9	15	14	US-10-161-791-306
43	28	33.3	8	14	US-10-008-524A-26
44	28	33.3	8	14	US-10-008-524A-27
45	28	33.3	8	14	US-10-008-524A-28

ALIGNMENTS

RESULT 1

US-09-938-315-92
; Sequence 92, Application US/09938315
; Patent No. US20020091085A1
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; SPARKS, ANDREW B.
; THORN, JUDITH M.
; QUILLIAM, LAWRENCE A.
; DER, CHANNING J.
; TITLE OF INVENTION: SIC SH3 BINDING PEPTIDES AND METHODS OF ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,315
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR


```

; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 255:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-255

Query Match 40.5%; Score 34; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
Db 3 PRPLPV 8

RESULT 6
US-10-161-791-410
; Sequence 410, Application US/10161791
; Publication No. US2003018683A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.

```

```

; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 410:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-410

Query Match 40.5%; Score 34; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
Db 4 PRPLPV 9

RESULT 7
US-09-938-315-86
; Sequence 86, Application US/09938315
; Patent No. US20020091085A1
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; APPLICANT: SPARKS, ANDREW B.
; APPLICANT: THORN, JUDITH M.
; APPLICANT: QUILLIAM, LAWRENCE A.
; APPLICANT: DER, CHANNING J.
; TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,315
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-938-315-86

Query Match 39.3%; Score 33; DB 9; Length 13;
Best Local Similarity 62.5%; Pred. NO. 2.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLPV 15
DB 2 TPRPLPML 9

RESULT 8
US-10-161-791-86
; Sequence 86, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIBER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-10-161-791-86

Query Match 39.3%; Score 33; DB 14; Length 13;
Best Local Similarity 62.5%; Pred. NO. 2.6e+02;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLPV 15
DB 2 TPRPLPML 9

RESULT 9
US-09-938-315-62
; Sequence 62, Application US/09938315
; Patent No. US20020091085A1
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; APPLICANT: SPARKS, ANDREW B.
; APPLICANT: THORN, JUDITH M.
; APPLICANT: QUILLIAM, LAWRENCE A.
; APPLICANT: DER, CHANNING J.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,315
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-09-938-315-62

Query Match 39.3%; Score 33; DB 9; Length 14;
Best Local Similarity 62.5%; Pred. NO. 2.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLPV 15
DB 3 TPRPLPML 10

RESULT 10
US-10-161-791-62
; Sequence 62, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.

```

; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-62

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```

Query Match      39.3%; Score 33; DB 14; Length 14;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY      8 SPRPLPVV 15
        :|||||:
DB      3 TERPLPML 10

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RESULT 11
US-10-161-791-378
; Sequence 378, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 378:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-378

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Query Match      38.7%; Score 32.5; DB 14; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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```

QY      1 CRAHSFGSPRPL 12
        :|||:
DB      4 CRALP-GEPRPL 14

```

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RESULT 12
US-10-059-261-8
; Sequence 8, Application US/10059261
; Publication No. US20030077826A1
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS
; APPLICANT: BRIAND, JEAN-PAUL
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOTENIC
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
; TITLE OF INVENTION: (PTPC)
; FILE REFERENCE: 03495.0216
; CURRENT APPLICATION NUMBER: US/10/059,261
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/265,594
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vector pACgp67-ScFv461
; OTHER INFORMATION: peptide sequence
US-10-059-261-8

```

```

Query Match      38.1%; Score 32; DB 14; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      1 CRAHSFGSPR 10
        :|||:
DB      1 CYVYAFGPR 10

```

```

RESULT 13

```

US-10-059-261-116
; Sequence 116, Application US/10059261
; Publication No. US20030077826A1
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS
; APPLICANT: BRIAND, JEAN-PAUL
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOTIC
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
; TITLE OF INVENTION: (PTPC)
; FILE REFERENCE: 03495.0216
; CURRENT APPLICATION NUMBER: US/10/059,261
; PRIOR FILING DATE: 2002-08-29
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 116
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vector pAcGp67-ScFv350
; OTHER INFORMATION: peptide sequence
US-10-059-261-116

Query Match 38.1%; Score 32; DB 14; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRAHSGSPR 10
Db 1 CYVYAGFPR 10

RESULT 14
US-09-938-315-67
; Sequence 67, Application US/09938315
; Patent No. US20020091085A1
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; SPARKS, ANDREW B.
; THORN, JUDITH M.
; QUILLIAM, LAWRENCE A.
; DER, CHANNING J.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,315
; FILING DATE: 23-Aug-2001
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-938-315-67

Query Match 36.9%; Score 31; DB 9; Length 14;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRPLP 13
Db 3 TPRPLP 8

RESULT 15
US-10-161-791-67
; Sequence 67, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-67

Query Match 36.9%; Score 31; DB 14; Length 14;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SPRPLP 13
:|||||
Db 3 TERPLP 8

Search completed: April 2, 2004, 10:23:35
Job time : 33.3333 secs

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OM protein - protein search, using sw model

Run on: April 2, 2004, 09:56:18 ; Search time 46 seconds
(without alignments)
92.135 Million cell updates/sec

Title: US-10-009-049-2

Perfect score: 79

Sequence: 1 SRAHFGSPRLPVV 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 447529

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	15	4	AAB59250 Peptide #
2	75	94.9	15	4	AAB59249 Peptide r
3	66	83.5	15	4	AAB59251 Peptide #
4	38	48.1	15	6	ABR44350 N-termina
5	37	46.8	15	5	AABW05069 Proline-r
6	36	45.6	15	5	ABG72660 Human K-r
7	35	44.3	13	2	AAW11111 Src SH3 d
8	34	43.0	9	2	AAW94619 Src homol
9	34	43.0	15	2	AAW39011 Peptide r
10	33	41.8	13	2	AAW11105 Src SH3 d
11	33	41.8	14	2	AAW11098 Src SH3 d
12	33	41.8	14	2	AAW25512 SH3 synth
13	33	41.8	14	4	AAW53295 Human non
14	32	40.5	10	4	AAW06985 CYP1B1 HL
15	32	40.5	10	4	AAW08385 HLA-A *02
16	32	40.5	10	4	AAW12350 HLA-A26 d
17	32	40.5	10	4	AAW08833 HLA-A1 de
18	32	40.5	10	4	AAW09489 HLA-B *07
19	32	40.5	11	5	AAW075613 Human non
20	32	40.5	12	3	AAW21272 ADAM 10/K
21	32	40.5	14	1	AAP60604 Sequence
22	31	39.2	10	2	AAR93295 fyn prote
23	31	39.2	10	2	AAR93312 PI3K prot
24	31	39.2	14	2	AAW11099 Src SH3 d
25	31	39.2	14	2	AAW25517 SH3 synth

26	31	39.2	14	4	AAM98385 Human pep
27	31	39.2	14	4	AAM98384 Human pep
28	31	39.2	15	2	AABW05068 Proline-r
29	30	38.0	8	4	ABW56489 Human sin
30	30	38.0	8	4	AAM13030 HLA-A *02
31	30	38.0	8	4	AAM11185 HLA-A *02
32	30	38.0	8	4	AAM10775 HLA-B8 oc
33	30	38.0	8	4	AAM09513 HLA-B8 oc
34	30	38.0	9	4	AAM08460 HLA-B *27
35	30	38.0	9	4	AAM12240 HLA-A26 n
36	30	38.0	9	4	AAM11714 HLA-A26 n
37	30	38.0	9	4	AAM12099 HLA-A *02
38	30	38.0	9	4	AAM08694 HLA-B *27
39	30	38.0	9	4	AAM11998 HLA-B *15
40	30	38.0	9	4	AAM11458 HLA-A26 n
41	30	38.0	9	4	AAM12119 HLA-A26 n
42	30	38.0	9	4	AAM08347 HLA-A1 no
43	30	38.0	9	4	AAM11149 HLA-B8 no
44	30	38.0	9	4	AAM07735 HLA-B *27
45	30	38.0	9	4	AAM07040 HLA-B *07

ALIGNMENTS

RESULT 1
AAB59250
ID AAB59250 standard; peptide; 15 AA.
XX
AC AAB59250;
XX
DT 27-MAR-2001 (first entry)
XX
DE Peptide #2 recognised by gene VIII library clone 45.
XX
KW Fibrin fragment E; cell proliferation; cancer; vascular restenosis;
KW arthritis; diabetes; renal disease; psoriasis.
XX
OS Synthetic.
XX
PN WO200075175-A1.
XX
PD 14-DEC-2000.
XX
PF 07-JUN-2000; 2000WO-GB002197.
XX
PR 07-JUN-1999; 99GB-00012994.
XX
(UVAB-) UNIV ABERDEEN.
PI Melvin WT, Thompson WD, Stirk CM;
XX
DR WPI; 2001-080581/09.
XX
PT New peptides capable of modulating a fibrin fragment E activity, useful
PT for inhibiting uncontrolled cell proliferation, e.g. for treating cancer,
PT vascular restenosis, atherosclerosis or psoriasis, and for wound healing.
XX
PS Claim 1; Page 49; 59pp; English.
XX
CC The present invention relates to a peptide or its fragment, which is
CC capable of modulating a fibrin fragment E activity. The peptides and
CC modulators are useful for inhibiting stimulation of cell proliferation
CC induced by a fibrin degradation product. The antibody or binding fragment
CC is also useful for identifying the active site of the fibrin fragment E
CC receptor. The peptides are particularly useful in treating cancer,
CC vascular restenosis, rheumatoid arthritis, diabetes, renal diseases or
CC psoriasis. The antibodies are also useful for modulating the activity of
CC the peptide

Sequence 15 AA;

Query Match 100.0%; Score 79; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHFGSPRPLPVV 15
DB 1 SRAHFGSPRPLPVV 15

RESULT 2
AAB59249
ID AAB59249 standard; peptide; 15 AA.
XX AC AAB59249;
XX DT 27-MAR-2001 (first entry)
XX DE Peptide recognised by gene VIII library clone 45.
XX KW Fibrin fragment E; cell proliferation; cancer; vascular restenosis;
XX KW arthritis; diabetes; renal disease; psoriasis.
XX OS Synthetic.
XX PN WO200075175-A1.
XX PD 14-DEC-2000.
XX PF 07-JUN-2000; 2000WO-GB002197.
XX PR 07-JUN-1999; 99GB-00012994.
XX PA (UYAB-) UNIV ABERDEEN.
XX PI Melvin WT, Thompson WD, Stirk CM;
XX DR WPI; 2001-080581/09.
XX PT New peptides capable of modulating a fibrin fragment E activity, useful
PT for inhibiting uncontrolled cell proliferation, e.g. for treating cancer,
PT vascular restenosis, atherogenesis or psoriasis, and for wound healing.
XX PS Claim 1; Page 49; 59pp; English.
XX CC The present invention relates to a peptide or its fragment, which is
CC capable of modulating a fibrin fragment E activity. The peptides and
CC modulators are useful for inhibiting stimulation of cell proliferation
CC induced by a fibrin degradation product. The antibody or binding fragment
CC is also useful for identifying the active site of the fibrin fragment E
CC receptor. The peptides are particularly useful in treating cancer,
CC vascular restenosis, rheumatoid arthritis, diabetes, renal diseases or
CC psoriasis. The antibodies are also useful for modulating the activity of
CC the peptide
XX SQ Sequence 15 AA;

Query Match 94.9%; Score 75; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAHSGSPRPLPVV 15
DB 2 RAHSGSPRPLPVV 15

RESULT 3
AAB59251
ID AAB59251 standard; peptide; 15 AA.
XX AC AAB59251;
XX DT 27-MAR-2001 (first entry)
XX DE Peptide #3 recognised by gene VIII library clone 45.

XX KW Fibrin fragment E; cell proliferation; cancer; vascular restenosis;
KW arthritis; diabetes; renal disease; psoriasis.
XX OS Synthetic.
XX PN WO200075175-A1.
XX PD 14-DEC-2000.
XX PF 07-JUN-2000; 2000WO-GB002197.
XX PR 07-JUN-1999; 99GB-00012994.
XX PA (UYAB-) UNIV ABERDEEN.
XX PI Melvin WT, Thompson WD, Stirk CM;
XX DR WPI; 2001-080581/09.
XX PT New peptides capable of modulating a fibrin fragment E activity, useful
PT for inhibiting uncontrolled cell proliferation, e.g. for treating cancer,
PT vascular restenosis, atherogenesis or psoriasis, and for wound healing.
XX PS Claim 1; Page 49; 59pp; English.
XX CC The present invention relates to a peptide or its fragment, which is
CC capable of modulating a fibrin fragment E activity. The peptides and
CC modulators are useful for inhibiting stimulation of cell proliferation
CC induced by a fibrin degradation product. The antibody or binding fragment
CC is also useful for identifying the active site of the fibrin fragment E
CC receptor. The peptides are particularly useful in treating cancer,
CC vascular restenosis, rheumatoid arthritis, diabetes, renal diseases or
CC psoriasis. The antibodies are also useful for modulating the activity of
CC the peptide
XX SQ Sequence 15 AA;

Query Match 83.5%; Score 66; DB 4; Length 15;
Best Local Similarity 92.9%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RAHSGSPRPLPVV 15
DB 2 RAHSGSPRPLPVV 15

RESULT 4
ABR44350
ID ABR44350 standard; peptide; 15 AA.
XX AC ABR44350;
XX DT 14-JUL-2003 (first entry)
XX DE N-terminal sequence for guanosine triphosphate activator 10.01.
XX KW Guanosine triphosphatase activator 10.01; squamous cell;
KW carcinoma of skin; osteosarcoma; leukemia; teratoma.
XX OS Unidentified.
XX PN CN1380320-A.
XX PD 20-NOV-2002.
XX PF 10-APR-2001; 2001CN-00105912.
XX PR 10-APR-2001; 2001CN-00105912.
XX PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX PI Mao Y, Xie Y;

XX WPI; 2003-222552/22.
 DR A polypeptide-guanosine triphosphatase activator protein -10.01 and
 XX polynucleotide for coding this polypeptide.
 PS Example 6; Page 21; 33pp; Chinese.
 XX The present invention discloses a polypeptide-guanosine triphosphatase
 CC activator protein-10.01. The invention also discloses the method for
 CC curing several diseases, such as squamous cell carcinoma of skin,
 CC osteosarcoma, leukemia and teratoma by using said polypeptide. The
 CC present sequence represents the N-terminal sequence of guanosine
 CC triphosphatase activator protein 10.01
 XX Sequence 15 AA;
 SQ

Query Match 48.1%; Score 38; DB 6; Length 15;
 Best Local Similarity 70.0%; Pred. No. 36;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 HSFQSPRLP 13
 |||||
 Db 4 HSLGSLQLP 13

RESULT 5
 AAW05069
 ID AAW05069 standard; peptide; 15 AA.
 XX
 AC AAW05069;
 XX
 DT 25-MAR-2003 (revised)
 DT 17-DEC-1996 (first entry)
 XX
 DE Proline-rich SH3 binding peptide fuse5B-4.51 from random library.
 XX
 KW Src homology domain; SH3 domain; oncogene; consensus;
 KW random display library.
 XX
 OS Synthetic.
 XX
 EH Key Location/Qualifiers
 FT 7.13
 FT /label= SH3 binding motif
 FT /note= "corresponds to consensus sequence RPLPXXP"
 XX
 US5541109-A.
 XX
 30-JUL-1996.
 XX
 19-APR-1994; 94US-00230047.
 XX
 19-APR-1994; 94US-00230047.
 XX
 (RHON) RHONE POULENC RORER PHARM INC.
 XX
 Ivashchenko YD, Ricca GA, Cheadle C, South VJ, Jaye MC;
 PI French SM, Searfoss GH;
 XX
 WPI; 1996-361965/36.
 XX
 New DNA encoding proteins that bind to Src-homology domain 3 - used to
 FT inhibit signal transduction, e.g. in cases of T cell activation.
 XX
 Example 1; Col 7; 39pp; English.
 PS
 CC A fusion phage library for expressing random 15mer peptides was prepared
 CC using the filamentous bacteriophage fuse 5B. The display library was
 CC screened for peptides which bind to the Src SH3 domain. A sequence
 CC comparison of the positive peptides revealed a highly reiterated, proline
 CC -rich, 7 amino acid consensus motif (i.e. the sequence RPLPXXP). This
 CC motif demonstrated a strong similarity to a Src SH3 binding sequence

CC identified within a protein isolated by screening a lambda-lox mouse
 CC embryo cDNA library with a Src SH3 domain probe. The present sequence is
 CC that of one of the positive peptides identified from the fuse 5B random
 CC display library. (Updated on 25-MAR-2003 to correct PI field.)
 XX Sequence 15 AA;
 SQ

Query Match 46.8%; Score 37; DB 2; Length 15;
 Best Local Similarity 70.0%; Pred. No. 51;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 HSFQSPRLP 13
 |||||
 Db 1 HSHFHPRLP 10

RESULT 6
 ABG72660
 ID ABG72660 standard; peptide; 15 AA.
 XX
 AC ABG72660;
 XX
 DT 26-FEB-2003 (first entry)
 XX
 DE Human K-ras 10.67 proto-oncogene protein, N-terminus.
 XX
 KW Human; K-ras 10.67; proto-oncogene; tumour; haemopathy;
 KW development disorder; human immunodeficiency virus infection; HIV;
 KW immunological disease; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN CN1352063-A.
 XX
 PD 05-JUN-2002.
 XX
 PF 02-NOV-2000; 2000CN-00127155.
 XX
 PR 02-NOV-2000; 2000CN-00127155.
 XX
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-658691/71.
 XX
 PT New human K-ras proto-oncogene protein 10.67 polypeptide for treating
 PT malignant tumors, hemopathy, development disorder, human immunodeficiency
 PT virus infection, immunological diseases and various inflammations.
 XX
 PS Example 5; Page 19 (disclosure); 33pp; Chinese.
 XX
 CC The present invention discloses a new kind of polypeptide, human K-ras
 CC proto-oncogene protein 10.67, polynucleotides encoding the polypeptide
 CC and a DNA recombination process to produce the polypeptide. The present
 CC invention also discloses applying the polypeptide in treating various
 CC diseases, such as malignant tumors, haemopathy, developmental disorder,
 CC human immunodeficiency virus (HIV) infection, immunological diseases and
 CC various inflammations. The present invention also discloses the
 CC antagonist resisting the polypeptide and its treatment effect. The
 CC present invention also discloses application of the polynucleotides
 CC encoding human K-ras proto-oncogene protein 10.67. The present sequence
 CC represents human K-ras proto-oncogene protein 10.67, N-terminus, used in
 CC an ELISA (enzyme-linked immunosorbent assay) experiment
 XX
 SQ Sequence 15 AA;

Query Match 45.6%; Score 36; DB 5; Length 15;
 Best Local Similarity 85.7%; Pred. No. 74;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSPRLP 13
 |||||

Db 8 GSPQPLP 14

RESULT 7
AAW11111
ID AAW11111 standard; peptide; 13 AA.
AC AAW11111;
XX 25-JUN-1997 (first entry)
DT Src SH3 domain-binding peptide used in signal transduction modulation.
DE Src; SH3; Src homology region 3; binding affinity; oncogenic protein;
XX protein tyrosine kinase; signal transduction; RNA processing;
KW trafficking; translation.
XX Synthetic.
OS
XX WO9603649-A1.
PN 08-FEB-1996.
PD
XX 24-JUL-1995; 95WO-US009382.
XX 22-JUL-1994; 94US-00278865.
PR 07-JUN-1995; 95US-00483555.
XX (UUNC-) UNIV NORTH CAROLINA.
PA
XX Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CJ;
FI WPI, 1996-117151/12.
XX Peptide with binding affinity for Src homology region 3 (SH3) domains of
PT proteins - useful for e.g. modulating signal transduction pathways at the
PT cellular level, esp. protein tyrosine kinase-mediated.
XX Claim 38; Page 87; 116pp; English.
PS
XX AAW1098-W1124 are peptides that bind to the Src SH3 domain. The SH3
CC binding peptides are useful in modulating signal transduction pathways at
CC the cellular level (especially protein tyrosine kinase-mediated),
CC modulating oncogenic protein activity, or providing compounds for the
CC development of drugs with the ability to modulate broad classes, as well
CC as specific classes, of proteins involved in signal transduction and also
CC for regulating the processing, trafficking or translation of RNA.
CC Conjugates of the peptides with detectable labels or imaging agents are
CC useful for imaging cells, tissues and organs in which Src or Src-related
CC proteins are expressed
XX Sequence 13 AA;
SQ

Query Match 44.3%; Score 35; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 92;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 SPRLPVV 15
:|||||:
Db 2 TPRLPLI 9

RESULT 8
AAW94619
ID AAW94619 standard; peptide; 9 AA.
XX
AC AAW94619;
XX 29-APR-1999 (first entry)
DT Src homology 3 domain binding nonamer peptide #1.
DE Src homology 3 domain; SH3 domain; peptidomimetic; mimetic; modulator;
KW

KW beta-turn template; spiro[pyrrolidine-2':3'-piperidin-2-ones],
KW fused ring analogue; signal transduction protein interaction;
XX inhibit cell growth; infection; cancer.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "acetylated"
XX
XX WO9854208-A1.
XX 03-DEC-1998.
XX 28-MAY-1998; 98WO-US010861.
XX 28-MAY-1997; 97US-00864241.
PR 18-MAY-1998; 98US-0085889P.
XX (CADU-) CADUS PHARM CORP.
XX Castelhano AL, Witter DJ;
XX WPI, 1999-080804/07.
XX spiro[pyrrolidine-2':3'-piperidin-2-ones] and their fused ring analogues -
PT used, e.g. to modulate signal transduction protein interactions, inhibit
PT cell growth and for use in treating infections and cancer.
XX Example 12; Page 59; 73pp; English.
PS
XX The present invention describes spiro[pyrrolidine-2':3'-piperidin-2-ones],
CC their fused ring analogues, and salts of both, all as individual
CC compounds or their libraries. They are peptidomimetics, and interact with
CC protein Src homology 3 (SH3) domains, involved in protein-protein
CC interactions in signal transduction. They cause disruption of the pathway
CC ; in particular, they inhibit the protein tyrosine kinase system involved
CC in cell growth regulation. The cells may be microbial, e.g. pathogenic
CC bacterial or fungal cells responsible for infections, or of transformed
CC cells, e.g. responsible for neoplastic conditions. Specific examples of
CC Src proteins with SH3 domains are those known by the abbreviations p85,
CC Fyn, Lyn, Hck, Syk, Grb2, Gap, STAP, p47-phox, p67-phox, and Bcr. The
CC present sequence represents a nonamer peptide used in an example from the
XX present invention
XX Sequence 9 AA;
SQ

Query Match 43.0%; Score 34; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPLPV 14
|||||
Db 1 PRPLPV 6

RESULT 9
AAW39011
ID AAW39011 standard; peptide; 15 AA.
XX
XX AAW39011;
XX 27-MAR-1998 (first entry)
DT Peptide resembling an SH3 domain binding peptide SEQ ID NO:410.
DE
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl;
KW PLCgamma; p53bp2; Crk; Yes; Grb2.
XX Synthetic.
OS
XX WO9730074-A1.
PN

The present sequence represents a Src SH3 synthetic binding peptide. SH3 (Src homology region 3) binding peptides are selected from: (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which bind the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i) peptides which bind the amino-terminal SH3 domain of Grb2. The purified binding peptides can be used in the method to identify inhibitors of their binding to their respective SH3 domains, which could be used to modulate the pharmacological activity of proteins or polypeptides containing the SH3 domain. The peptides can also be used to activate Src or Src-related

Query Match 41.8%; Score 33; DB 4; Length 14;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 SPRPLPV 14
| | | | |
Db 6 SPRPAPV 12

RESULT 14

AAM06985
ID AAM06985 standard; peptide; 10 AA.

XX AC AAM06985;

XX DT 09-OCT-2001 (first entry)

XX DE CYP1B1 HLA-A2 binding peptide fragment #35.

XX KW Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA;
XX KW human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; APC;
XX KW major histocompatibility complex; antigen presenting cell; melanoma;
XX KW lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.

XX OS Homo sapiens.

XX PN WO200135810-A2.

XX PD 25-MAY-2001.

XX PF 15-NOV-2000; 2000WO-US031513.

XX PR 15-NOV-1999; 99US-0165590P.

XX PA (DAND) DANA FARBER CANCER INST INC.
XX PA (UYBO-) UNIV BOSTON.

XX PI Schultze JL, Vonderheide RH, Sherr D, Nadler LM, Maecker B;
XX PI Von Bergwelt-Baildon M;

XX DR WPI; 2001-355537/37.

XX PT Treating a cancer patient involves administering to patient a cytotoxic T
XX PT -lymphocyte, an antigen presenting cell that activates T cells, a peptide
XX PT of cytochrome P450 1B1, or a polynucleotide encoding the peptide.

XX PS Disclosure; Page 40; 121pp; English.

XX CC The present invention describes a method for treating a patient having,
XX CC or is at risk of having, a cell expressing cytochrome P450 1B1 (CYP1B1),
XX CC which involves administering to the patient a cytotoxic T-lymphocyte
XX CC (CTL) that kills the cell, an antigen presenting cell (APC) that
XX CC activates CTL, a peptide of CYP1B1 that binds to major histocompatibility
XX CC complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or
XX CC peptide of CYP1B1. Also described are: (1) a method for assessing the
XX CC level of immunity of a patient to CYP1B1 or a peptide of CYP1B1 that
XX CC binds to MHC complex molecule, involving measuring the level of CTL
XX CC specific for CYP1B1 or the peptide of CYP1B1 in a sample from the patient
XX CC ; (2) a CYP1B1 peptide (I) that binds to MHC complex molecule; (3) an ex
XX CC vivo generated CTL (II) that specifically kills a cell expressing CYP1B1
XX CC in a specific of a MHC complex-restricted fashion; and (4) an ex vivo
XX CC generated APC (III) that presents a peptide of a CYP1B1 in the context of
XX CC a MHC complex molecule. The method is useful for treating a patient
XX CC having or is at risk of having a cell that expresses CYP1B1. The method
XX CC is useful for the prevention, treatment and diagnosis of cancer, e.g.
XX CC melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and
XX CC lung, ovarian, uterine, cervical, prostate, liver, colon, pancreatic and
XX CC brain cancer. AAM06905 to AAM13566 represent CYP1B1 peptides which can
XX CC bind to human leukocyte antigens (HLAs), as well as other amino acid
XX CC sequence used in the exemplification of the present invention

XX SQ Sequence 10 AA;

Query Match 40.5%; Score 32; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGSPRLPVV 15
| | | | |
Db 1 FLDPRPLTVV 10

RESULT 15

AAM08985

ID AAM08985 standard; peptide; 10 AA.

XX AC AAM08985;

XX DT 09-OCT-2001 (first entry)

XX DE HLA-A *0201 decamer #2.

XX KW Cytochrome P450 1B1; CYP1B1; cancer; immunotherapy; diagnosis; HLA;
XX KW human leukocyte antigen; cytotoxic T-lymphocyte; CTL; MHC; APC;
XX KW major histocompatibility complex; antigen presenting cell; melanoma;
XX KW lymphoma; carcinoma; sarcoma; multiple myeloma; leukaemia.

XX OS Homo sapiens.

XX PN WO200135810-A2.

XX PD 25-MAY-2001.

XX PF 15-NOV-2000; 2000WO-US031513.

XX PR 15-NOV-1999; 99US-0165590P.

XX PA (DAND) DANA FARBER CANCER INST INC.
XX PA (UYBO-) UNIV BOSTON.

XX PI Schultze JL, Vonderheide RH, Sherr D, Nadler LM, Maecker B;
XX PI Von Bergwelt-Baildon M;

XX DR WPI; 2001-355537/37.

XX PT Treating a cancer patient involves administering to patient a cytotoxic T
XX PT -lymphocyte, an antigen presenting cell that activates T cells, a peptide
XX PT of cytochrome P450 1B1, or a polynucleotide encoding the peptide.

XX PS Disclosure; Page 69; 121pp; English.

XX CC The present invention describes a method for treating a patient having,
XX CC or is at risk of having, a cell expressing cytochrome P450 1B1 (CYP1B1),
XX CC which involves administering to the patient a cytotoxic T-lymphocyte
XX CC (CTL) that kills the cell, an antigen presenting cell (APC) that
XX CC activates CTL, a peptide of CYP1B1 that binds to major histocompatibility
XX CC complex (MHC) molecule, or a nucleic acid molecule encoding CYP1B1 or
XX CC peptide of CYP1B1. Also described are: (1) a method for assessing the
XX CC level of immunity of a patient to CYP1B1 or a peptide of CYP1B1 that
XX CC binds to MHC complex molecule, involving measuring the level of CTL
XX CC specific for CYP1B1 or the peptide of CYP1B1 in a sample from the patient
XX CC ; (2) a CYP1B1 peptide (I) that binds to MHC complex molecule; (3) an ex
XX CC vivo generated CTL (II) that specifically kills a cell expressing CYP1B1
XX CC in a specific of a MHC complex-restricted fashion; and (4) an ex vivo
XX CC generated APC (III) that presents a peptide of a CYP1B1 in the context of
XX CC a MHC complex molecule. The method is useful for treating a patient
XX CC having or is at risk of having a cell that expresses CYP1B1. The method
XX CC is useful for the prevention, treatment and diagnosis of cancer, e.g.
XX CC melanoma, lymphoma, carcinoma, sarcoma, multiple myeloma, leukemia, and
XX CC lung, ovarian, uterine, cervical, prostate, liver, colon, pancreatic and
XX CC brain cancer. AAM06905 to AAM13566 represent CYP1B1 peptides which can
XX CC bind to human leukocyte antigens (HLAs), as well as other amino acid
XX CC sequence used in the exemplification of the present invention

XX SQ Sequence 10 AA;

Query Match 40.5%; Score 32; DB 4; Length 10;
 Best Local Similarity 70.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FGSRPRLPVV 15
 | | | | |
 Db 1 FLDPRLTVV 10

Search completed: April 2, 2004, 10:08:42
 Job time : 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 10:05:03 ; Search time 11 seconds
(without alignments)
131.170 Million cell updates/sec

Title: US-10-009-049-2

Perfect score: 79

Sequence: 1 SRAHSFGSPRLPVV 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2522

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	34.2	14	2 S27140	hypothetical prote
2	26	32.9	13	1 XAVI9B	angiotensin-conver
3	26	32.9	13	2 PA0089	protein QP200053 -
4	24	30.4	11	2 C37196	bradykinin-potenti
5	24	30.4	11	2 D37196	bradykinin-potenti
6	24	30.4	12	2 S43170	kinesin light chai
7	24	30.4	14	2 PA0013	photosystem II oxy
8	23	29.1	12	2 PH1457	T-cell receptor be
9	23	29.1	15	2 PA0060	protein QP200037 -
10	22.5	28.5	15	2 P50452	32K protein 3306 -
11	22	27.8	7	2 S36662	dermorphin (Iys-7)
12	22	27.8	8	2 D47393	neuropeptide calla
13	22	27.8	13	2 PL0157	Ig kappa chain V-1
14	22	27.8	14	2 G44957	photosystem II oxy
15	21.5	27.2	13	2 I84603	deoxynucleotidyltr
16	21	26.6	9	2 P70238	Ig heavy chain CRD
17	21	26.6	13	2 B61620	locustamytropin I
18	21	26.6	15	2 A22789	platelet-derived g
19	20	25.3	7	1 A61324	dermorphin - Rohde
20	20	25.3	8	2 J50316	leucokinin VI - Ma
21	20	25.3	9	4 S15594	orf 1 rara 5'-regi
22	20	25.3	10	2 PX0030	triacylglycerol li
23	20	25.3	11	2 I33098	173K exoantigen -
24	20	25.3	12	2 S01122	photosystem II 3.7
25	20	25.3	12	2 PH1459	T-cell receptor be
26	20	25.3	12	2 PH1468	T-cell receptor be
27	20	25.3	12	4 PC2121	aminotransferase c
28	20	25.3	15	2 S59492	formate dehydrogen
29	20	25.3	15	2 A40634	orf19 3' of eryK -

30	20	25.3	15	2 B32800	hypothetical prote
31	20	25.3	15	2 PX0031	mixed lymphocyte r
32	19	24.1	9	2 A31576	xylose isomerase (
33	19	24.1	10	1 XAVI6B	angiotensin-conver
34	19	24.1	11	1 XASNBA	bradykinin-potenti
35	19	24.1	11	2 UN0023	substance P - chic
36	19	24.1	11	2 S23308	substance P - rain
37	19	24.1	11	2 S23306	substance P - Ala
38	19	24.1	11	2 E41476	probable antigen 5
39	19	24.1	11	2 S33300	probable substance
40	19	24.1	12	2 S26559	T-cell receptor be
41	19	24.1	12	2 S26554	T-cell receptor be
42	19	24.1	12	2 A37933	Ig lambda chain J
43	19	24.1	12	2 PH1467	T-cell receptor be
44	19	24.1	12	2 PH1462	T-cell receptor be
45	19	24.1	12	2 PH1469	T-cell receptor be

ALIGNMENTS

RESULT 1

S27140
hypothetical protein 1 estrogen receptor 5'-region - human
C:Species: Homo sapiens (man)
C:Date: 05-Mar-1994 #sequence_revision 12-May-1995 #text_change 18-Aug-2000
C:Accession: S27140
R:Keaveney, M.; Klug, J.; Gannon, F.
DNA Seq. 2, 347-358, 1992
A:Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene.
A:Reference number: S27140; MUID:93075998; PMID:1476547
A:Accession: S27140
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-14 <KEA>
A:Cross-references: EMBL:X62462; NID:g31201; PIDN:CAA44319.1; PID:g31202
C:Superfamily: unassigned leader peptides

Query Match 34.2%; Score 27; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAHSF 6
DB 2 RAHSF 6

RESULT 2

XAVI9B
angiotensin-converting enzyme inhibitor V-9 - jararaca
C:Species: Bothrops jararaca (jararaca)
C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995
C:Accession: A01253
R:Ondetti, M.A.; Williams, N.J.; Sabo, E.F.; Pluscec, J.; Weaver, E.R.; Kocy, O.
Biochemistry 10, 4033-4039, 1971
A:Title: Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. Is
A:Reference number: A90356; MUID:72118526; PMID:4334402
A:Accession: A01253
A:Molecule type: protein
A:Residues: 1-13 <OND>
A:Note: the structure of the peptide was confirmed by synthesis
C:Comment: This peptide also potentiates bradykinin by inhibiting the kinases that inacti
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 32.9%; Score 26; DB 1; Length 13;
Best Local Similarity 55.6%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 GSPRPLPVV 15
DB 3 GWPRPGPEI 11

RESULT 3

PA0089
protein QF200053 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0089
R;Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A;Reference number: PA0051
A;Accession: PA0089
A;Molecule type: protein
A;Residues: 1-13 <CHO>

Query Match 32.9%; Score 26; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSPRP 11

DB 5 GAPRP 9

RESULT 4

C37196
bradykinin-potentiating peptide 3 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C;Accession: C37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides 3
A;Reference number: A37196; PMID:90351557; PMID:2386615
A;Accession: C37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <CIN>
A;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 30.4%; Score 24; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GSPRP 11

DB 3 GPPRP 7

RESULT 5

D37196
bradykinin-potentiating peptide 4 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C;Accession: D37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides 4
A;Reference number: A37196; PMID:90351557; PMID:2386615
A;Accession: D37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <CIN>
A;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 30.4%; Score 24; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GSPRP 11

DB 3 GPPRP 7

RESULT 6

S43170
kinesin light chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: S43170
R;Chernajovsky, Y.; Brown, A.; Jones, T.A.; Sheer, D.
submitted to the EMBL Data Library, December 1992
A;Description: Promoter first exon/intron characterization and chromosomal location of tk
A;Reference number: S43170
A;Accession: S43170
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-12 <CHE>
A;Cross-references: EMBL:X69658; NID:g468786; PIDN:CAA49349.1; PID:g468787

Query Match 30.4%; Score 24; DB 2; Length 12;
Best Local Similarity 55.6%; Pred. No. 7.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 RAHSFGSPR 10

DB 3 RGGSGAPR 11

RESULT 7

PA0013
photosystem II oxygen-evolving complex protein 2 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C;Accession: PA0013
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional
A;Reference number: PA0001
A;Accession: PA0013
A;Molecule type: protein
A;Residues: 1-14 <KAM>
A;Experimental source: leaf
A;Keywords: photosynthesis; photosystem II

Query Match 30.4%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 AHSFGSPR 10

DB 6 ANVFKPK 13

RESULT 8

PH1457
T-cell receptor beta chain (clone A3/IC1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 17-Mar-1999
C;Accession: PH1457; S26542
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kou
J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH1457
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>
A;Experimental source: cytolytic T-lymphocyte, clone A3/IC1
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A;Reference number: S26512; MUID:92364546; PMID:1380061
A;Accession: S26542

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-12 <CA2>
 A:Cross-references: EMBL:X67992
 A:Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas2
 C:Superfamily: immunoglobulin homology
 C:Keywords: receptor; T-cell

Query Match 29.1%; Score 23; DB 2; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AHSFGS 8
 |||||
 DB 2 ASSFGS 7

RESULT 9

PA0060
 protein QP200037 - fungus (Fusarium sporotrichioides) (fragment)
 C:Species: Fusarium sporotrichioides
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C:Accession: PA0060
 R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
 A:Reference number: PA0051
 A:Accession: PA0060
 A:Molecule type: protein
 A:Residues: 1-15 <CHO>

Query Match 29.1%; Score 23; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 RPLP 13
 |||||
 DB 3 RPLP 6

RESULT 10

PS0452
 32K protein 3306 - rice (strain Nihonbare) (fragment)
 C:Species: Oryza sativa (rice)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
 C:Accession: PS0452
 R:Tsugita, A.; Miyatake, N.
 submitted to JIPID, April 1993
 A:Reference number: PS0208
 A:Accession: PS0452
 A:Molecule type: protein
 A:Residues: 1-15 <TSU>
 A:Experimental source: bran, strain Nihonbare
 C:Comment: molecular weight 32K, pI 5.3.

Query Match 28.5%; Score 22.5; DB 2; Length 15;
 Best Local Similarity 45.5%; Pred. No. 1.6e+03;
 Matches 5; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 5 SFGSPRPDPV 15
 |||||
 DB 3 SFG---PPFIL 10

RESULT 11

S36662
 dermorphin (lys-7) [validated] - two-colored leaf frog
 C:Species: Phyllomedusa bicolor (two-colored leaf frog)
 C:Date: 10-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 18-Aug-2000
 C:Accession: S36662
 R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Ersamer, G.; Kreil, G.
 FEBS Lett. 302, 151-154, 1992
 A:Title: Identification and characterization of two dermorphins from skin extracts of th

A:Reference number: S21152; MUID:92339502; PMID:1633846
 A:Accession: S36662
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <MIG>
 C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 27.8%; Score 22; DB 2; Length 7;
 Best Local Similarity 42.9%; Pred. No. 2.8e+05;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 HSPGSPR 10
 ::|||:
 DB 1 YAFGYPK 7

RESULT 12

D47393
 neuropeptide callatostatin 4 - bluebottle fly (Calliphora vomitoria)
 C:Species: Calliphora vomitoria
 C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995
 C:Accession: D47393
 R:Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.
 proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
 A:Title: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequen
 A:Reference number: A47393; MUID:93211980; PMID:8460157
 A:Accession: D47393
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <DUV>
 A:Experimental source: thoracic ganglia
 A:Note: sequence extracted from NCBI backbone (NCBIP:128479)

Query Match 27.8%; Score 22; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RAHSPG 7
 |::||
 DB 2 RPYSPG 7

RESULT 13

PL0157
 Ig kappa chain V-II region (anti-myelin-associated glycoprotein, PEC) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-Feb-1997
 C:Accession: PL0157; C61458
 R:Broutet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
 J. Exp. Med. 170, 1551-1558, 1989
 A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-asso
 A:Reference number: A61458; MUID:90039128; PMID:2478651
 A:Accession: PL0157
 A:Molecule type: protein
 A:Residues: 1-13 <BRO>
 A:Accession: C61458
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13 <BR2>
 C:Comment: This protein is one of monoclonal IgM reactive with myelin-associated glycopr
 C:Keywords: glycoprotein; heterotetramer; immunoglobulin

Query Match 27.8%; Score 22; DB 2; Length 13;
 Best Local Similarity 71.4%; Pred. No. 1.6e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 SPRPLPV 14
 |||||
 DB 7 SPVTLPV 13

RESULT 14

G44957

photosystem II oxygen-evolving complex protein 2 - common tobacco (cv. Samsun NN) (fragment)
C/Species: Nicotiana tabacum (common tobacco)
C/Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Jun-1993
C/Accession: G44957

R/Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.
Plant Cell Physiol. 31, 215-221, 1990
A/Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabacum
A/Reference number: A44957
A/Accession: G44957
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-14 <TAK>

Query Match 27.8%; Score 22; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AHSEFGSP 9
| : |||
Db 6 ANVEGKP 12

RESULT 15

I84603
deoxynucleotidyltransferase - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C/Accession: I84603
R/Koizumi, O.; Kaneda, T.; Morishita, R.
Biochem. Biophys. Res. Commun. 144, 185-190, 1987
A/Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in man
A/Reference number: I45884; MUID:87213162; PMID:3579900
A/Accession: I84603
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-13 <RES>
A/Cross-references: GB:M26144; NID:g951194; PIDN:AAA74588.1; PID:g951195
C/Genetics:
A/Gene: GDB:DNTT
A/Cross-references: GDB:119100; OMIM:187410
A/Map position: 10q23-10q24

Query Match 27.2%; Score 21.5; DB 2; Length 13;
Best Local Similarity 45.5%; Pred. No. 2e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 7 GSP---RPLPV 14
| : |||
Db 2 GQPDGRQPLEM 12

Search completed: April 2, 2004, 10:11:51
Job time : 11 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 2, 2004, 09:58:38 ; Search time 7.66667 Seconds
(without alignments)
101.876 Million cell updates/sec

Title: US-10-009-049-2
Perfect score: 79
Sequence: 1 SRAHSFGSPRLPVV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 801

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	26	32.9	8	1 ALL3_CYDPO	P82154 cydia pomon
2	26	32.9	13	1 BPP1_BOTJA	P01020 bothrops ja
3	26	32.9	15	1 UC29_MAIZE	P80635 zea mays (m
4	25	31.6	13	1 PSBP_PINPS	P81658 pinus pinas
5	24	30.4	11	1 BPP2_BOTIN	P30423 bothrops in
6	24	30.4	11	1 BPP4_BOTIN	P30424 bothrops in
7	24	30.4	15	1 MK1_PALPR	P80408 palomena pr
8	24	30.4	15	1 MK2A_PALPR	P80409 palomena pr
9	23	29.1	8	1 ALL4_CYDPO	P82155 cydia pomon
10	23	29.1	9	1 FAR9_ASCSU	P43172 ascaris suu
11	23	29.1	12	1 FSP3_PHYPA	P80662 physcomitre
12	22	27.8	8	1 ALL4_CALVO	P41840 calliphora
13	22	27.8	10	1 FAR6_PANRE	P82660 panagrellus
14	21	26.6	11	1 TIN4_HOPTI	P82654 hoplobatr
15	21	26.6	12	1 PK4_PBRFU	P82630 periplaneta
16	21	26.6	12	1 TIN2_HOPTI	P82652 hoplobatr
17	21	26.6	12	1 TIN3_HOPTI	P82653 hoplobatr
18	21	26.6	13	1 LMT4_LOOMI	P41490 locusta mig
19	21	26.6	14	1 EDCD_LYMDI	P80940 lymantria d
20	21	26.6	15	1 PDGB_PIG	P20034 sus scrofa
21	20	25.3	8	1 ALL5_CYDPO	P82156 cydia pomon
22	20	25.3	8	1 LCK6_LEUMA	P19988 leucophaea
23	20	25.3	9	1 MGMT_BOVIN	P29177 bos taurus
24	20	25.3	12	1 PK4_PERAM	P82619 periplaneta
25	20	25.3	15	1 METK_MAIZE	P80616 zea mays (m
26	19	24.1	7	1 ALL2_CARMA	P81805 carcinus ma
27	19	24.1	8	1 AL17_CARMA	P81820 carcinus ma
28	19	24.1	8	1 AL18_CARMA	P81821 carcinus ma
29	19	24.1	8	1 LCK4_LEUMA	P21143 leucophaea
30	19	24.1	9	1 XYLA_STRSQ	P19149 streptomyc
31	19	24.1	10	1 BPP2_BOTJA	P01022 bothrops ja
32	19	24.1	11	1 BPPB_AGHA	P01021 agkistrodon
33	19	24.1	11	1 TKNA_CHICK	P19850 gallus gall

34	19	24.1	11	1 TKNA_GADMO	P28498 gadus morhu
35	19	24.1	11	1 TKNA_ONCMY	P28499 oncorhynch
36	19	24.1	11	1 TKNA_SCYCA	P41333 scyllorhinu
37	19	24.1	14	1 UC15_MAIZE	P80621 zea mays (m
38	18	22.8	5	1 AL14_CARMA	P81817 carcinus ma
39	18	22.8	8	1 AL15_CARMA	P81818 carcinus ma
40	18	22.8	8	1 VGLG_HSV2B	P81780 herpes simp
41	18	22.8	10	1 AL19_CARMA	P81822 carcinus ma
42	18	22.8	10	1 FARP_MANSE	P18523 manduca sex
43	18	22.8	10	1 PNEU_RAT	P21996 rattus norv
44	18	22.8	13	1 TEMD_RANTE	P56919 rana tempor
45	18	22.8	14	1 RS19_CLOPP	Q46228 clover prol

ALIGNMENTS

RESULT 1
ALL3_CYDPO STANDARD; PRT; 8 AA.
AC P82154;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydia pomonella 3.
OC Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Dave H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -|- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 926 MW; C82879DSAB477415 CRC64;
AMIDATION

Query Match 32.9%; Score 26; DB 1; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.4e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SRAHSFG 7
DB 1 SRPYSFG 7

RESULT 2
BPP1_BOTJA STANDARD; PRT; 13 AA.
AC P01020; P30421;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S3,1 (13A) (Angiotensin-converting
enzyme inhibitor V-9).
OS Bothrops jararaca (Jararaca), and
OC Bothrops insularis (Island Jararaca) (Queimada Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724, 8723;
RN [1]
RP SEQUENCE.
RC SPECIES=B. jararaca; TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocy O.;

RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
 RT jararaca. Isolation, elucidation of structure, and synthesis.";
 RL Biochemistry 10:4033-4039(1971).
 RN [2]

RC SPECIES=B. insularis; TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).

CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.

DR PIR; A01253; XAVI9B.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 13 AA; 1388 MW; 6824FC97D83D6774 CRC64;

Query Match 32.9%; Score 26; DB 1; Length 13;
 Best Local Similarity 55.6%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 GSPRLPVV 15
 | | | | |
 Db 3 GWPFGPEI 11

RESULT 3

ID UC29 MAIZE STANDARD; PRT; 15 AA.
 AC P80635;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 45)
 DE (Fragment).
 OS Zea mays (Maize).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC PACAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Danerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 4.9, its MW is: 37.6 kDa.

DR Maize-2DPAGE; P80635; COLEOPTILE.
 DR MaizeDB; 123960; -.
 FT NON TER 1 1
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1679 MW; 3D53086B16018BC1 CRC64;
 Query Match 32.9%; Score 26; DB 1; Length 15;
 Best Local Similarity 42.9%; Pred. No. 2.2e+02;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 SPRPLPV 14
 | | | | |
 Db 1 NPNVPVI 7

RESULT 4

PSBP PINPS STANDARD; PRT; 13 AA.
 ID PSBP PINPS
 AC P81668;
 DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Oxygen-evolving enhancer protein 2 (OEE2) (23 kDa subunit of oxygen
 DE evolving system of photosystem II) (Fragment).
 RN PSBP.

OS Pinus pinaster (Maritime pine).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins.";
 RL Electrophoresis 20:1098-1108(1999).

CC -!- FUNCTION: May be involved in the regulation of photosystem II.
 CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
 CC with the photosystem II complex (By similarity).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
 CC (spot N179) is: 5.9, its MW is: 22 kDa.
 CC -!- SIMILARITY: Belongs to the psbp family.
 CC Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane.

KW NON_TER 13 13
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1294 MW; C6772B0D54D7C44D CRC64;

Query Match 31.6%; Score 25; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 AHSFGSPR 10
 | | | | |
 Db 6 ANVFGAPK 13

RESULT 5

ID BPP3 BOTIN STANDARD; PRT; 11 AA.
 AC P30423;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-PEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 CC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).

CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; C37196; C37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1199 MW; 20E25813C7741777 CRC64;

Query Match 30.4%; Score 24; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GSPRP 11

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SRAHSGF 7
:|:|:|
Db 1 ARPYSEF 7

RESULT 10

FAR9_ASCSU
ID FAR9_ASCSU STANDARD; PRT; 9 AA.
AC P43172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRPamide-like neuropeptide AF9.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoideus).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRPamide-like neuropeptides isolated from the nematode
RT Ascaris suum";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)
CC family.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 29.1%; Score 23; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PRPL 12
:|:|:|
Db 4 PRPL 7

RESULT 11

PSP3_PHYPA
ID PSP3_PHYPA STANDARD; PRT; 12 AA.
AC P80662;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oxygen-evolving enhancer protein 2 (OE2) (24 kDa subunit of oxygen
DE evolving system of photosystem II) (Fragment).
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP SEQUENCE.
RX TISSUE=Protonema;
RC MEDLINE=97275459; PubMed=9129336;
RA Kaestn B., Buck F., Nuske J., Reski R.;
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
RT plastid enzymes.";
RL Planta 201:261-272(1997).
CC -!- FUNCTION: May be involved in the regulation of photosystem II.
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
CC with the photosystem II complex.
CC -!- INDUCTION: By light.
CC -!- SIMILARITY: Belongs to the psbp family.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane;
KW Multigene family.
FT NON TER 12
SQ SEQUENCE 12 AA; 1182 MW; 8D280D54D7C44DC5 CRC64;

Query Match 29.1%; Score 23; DB 1; Length 12;

Best Local Similarity 57.1%; Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AHSFGSP 9
:|:|:|
Db 6 ANVEGAP 12

RESULT 12

ALL4_CALVO
ID ALL4_CALVO STANDARD; PRT; 8 AA.
AC P41840;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Callatostatin 4 (Leu-callatostatin 4).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX TISSUE=Thoracic ganglion;
RC MEDLINE=93211980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=94291167; PubMed=8020069;
RA Duve H., Thorpe A.;
RT "Distribution and functional significance of Leu-callatostatins in
RT the blowfly Calliphora vomitoria.";
RL Cell Tissue Res. 276:367-379(1994).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator and play
CC a role in the integration of information within the brain. May be
CC involved in the control of visceral muscles due to its ability to
CC behave as potent inhibitors of peristaltic movements. May also
CC fulfill a neurohormonal role on muscles of the gut and heart.
CC -!- TISSUE SPECIFICITY: Brain, suboesophageal ganglion, retrocerebral
CC complex, thoracic-abdominal ganglion, peripheral neurosecretory
CC system and intestine.
CC -!- SIMILARITY: Belongs to the allatostatin family.
DR PIR; D47393; D47393.
KW Neuropeptide; Amidation.
FT MOD RES 8
FT UNSURE 1
SQ SEQUENCE 8 AA; 954 MW; D32879D5AB47740A CRC64;

Query Match 27.8%; Score 22; DB 1; Length 8;

Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RAHSFG 7
:|:|:|
Db 2 RPYSEF 7

RESULT 13

FAR6_PANRE
ID FAR6_PANRE STANDARD; PRT; 10 AA.
AC P82660;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRPamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;


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RN SEQUENCE, FUNCTION, AND AMIDATION.
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA Maule A.G.;
RT "Isolation, characterization and pharmacology of RMRamide-related
RT peptides (RMRpe) from free-living nematode, Panagrellus redivivus."
RL Submitted (JUL-2000) to Swiss-Pat.
CC -!- FUNCTION: Myoactive.
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
KW Neuropeptide; Amidation.
FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 27.8%; Score 22; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 6.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSPRP 11
Db 2 GAPQP 6

RESULT 14
TIN4 HOPTI STANDARD; PRT; 11 AA.
AC P82654;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tigerin-4.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RN SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
TISSE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitarum N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina."
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
CC S.aureus, M.luteus, P.putida and S.cerevisiae.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 3 11
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 26.6%; Score 21; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PLPV 14
Db 7 PLPI 10

RESULT 15
PPK4 PERFU STANDARD; PRT; 12 AA.
AC P82690;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-4 (PEP-PK-4) (YXPRL-amide).
OS Periplaneta fuliginosa (Smokybrown cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=36977;
RN [1]
RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP TISSUE=Corpora cardiaca;
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of EXPRlamides in the nervous system of
RT the American cockroach."
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -!- MASS SPECTROMETRY: MW=1437.9; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the pyrokinin family.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1439 MW; F9B53049FF42CAA1 CRC64;

Query Match 26.6%; Score 21; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 AHSFGSPR 10
Db 4 SHDVYSR 11

Search completed: April 2, 2004, 10:09:17
Job time : 7.66667 secs

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